



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 163666

TO: John Ulm
Location: rem/4E79/4C70
Art Unit: 1649
Sept. 1, 2005

Case Serial Number: 10/719692

From: P. Sheppard
Location: Remsen Building
Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

THIS PAGE BLANK (USPTO)

From: Ulm, John
Sent: Wednesday, August 24, 2005 9:58 AM
To: STIC-Biotech/ChemLib
Subject: search SEQ ID NO:6 of application Serial Number 10/719,692

Please search SEQ ID NO:6 of application Serial Number 10/719,692.
John Ulm. 571 272-0880, Room REM 4E79, mail box REM 4C70, results prefered in paper.

Thank you.

SEARCHED
INDEXED
SERIALIZED
FILED
AUG 24 2005
CLERK'S OFFICE
U.S. DISTRICT COURT
N.D. OF ALABAMA

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2005, 18:20:50 ; Search time 166 Seconds
(without alignments)

806.139 Million cell updates/sec

Title: US-10-719-692-6

Perfect score: 1853

Sequence: 1 MYNGSCCR1EGDTLSQVMPP.....ANSFQSQSDGQWDDPHIVEWH 346

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105632

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqP1980s;*

2: geneseqP1990s;*

3: geneseqP2000s;*

4: geneseqP2001s;*

5: geneseqP2002s;*

6: geneseqP2003s;*

7: geneseqP2004s;*

8: geneseqP2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query Score Match Length DB ID Description

Result No.	Score	Match	Length	DB	ID	Description
1	100.0	346	4	AAGB0968		AAGB0968 Human nGP
2	100.0	346	4	ABBA4522		ABBA4522 Human GPC
3	100.0	346	4	AAU06197		AAU06197 Novel hum
4	100.0	346	4	AAU04373		AAU04373 Human G-P
5	100.0	346	5	AAE16172		AAE16172 Human G-P
6	100.0	346	5	AAU11401		AAU11401 HM74-like
7	100.0	346	5	AAE17077		AAE17077 Human G-P
8	100.0	346	5	ABB09596		ABB09596 Human LIP
9	100.0	346	5	ABG9786		ABG9786 Human G-P
10	100.0	346	5	ABP9599		ABP9599 Human GPC
11	100.0	346	5	AA014788		AA014788 Human pur
12	100.0	346	5	AAE24354		AAE24354 Human G-P
13	100.0	346	6	ABP81747		ABP81747 Human che
14	100.0	346	6	ABP56751		ABP56751 Human GAV
15	100.0	346	6	AAO26511		AAO26511 Human G-P
16	100.0	346	6	ABPS0453		ABPS0453 Human res
17	100.0	346	7	ADC46872		ADC46872 Human TA
18	100.0	346	7	ABW0810		ABW0810 Human GPC
19	100.0	346	7	ADE40282		ADE40282 Human NOV
20	100.0	346	7	ADE40272		ADE40272 Human NOV
21	100.0	346	7	ADE40278		ADE40278 Human NOV
22	100.0	346	7	ABW02123		ABW02123 Human GPC
23	100.0	346	7	ADI21235		ADI21235 Novel hum
24	100.0	346	7	ADL96470		ADL96470 Human G-P
25	100.0	346	8	ADJ71681		ADJ71681 Human NOV

ALIGNMENTS

RESULT 1
AAGB0968

ID AAGB0968 standard; protein; 346 AA.

XX
AC AAGB0968;
XX DT 28-AUG-2001 (first entry)
XX DE Human nGCPRII #2.
XX KW G protein-coupled receptor; nGPCR; seven transmembrane receptor;
KW signal transduction; schizophrenia; thyroid disorder; renal failure;
KW rheumatoid arthritis; CNS disorder; infection; metabolic disease;
KW cardiovascular disease; proliferative disorder; hormonal disorder;
KW neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
KW attention deficit-hyperactivity disorder; attention deficit disorder;
KW Parkinson's disease; migraine; senile dementia; inflammatory disease;
KW rheumatoid arthritis; autoimmune disorder; respiratory ailment;

KW neuroprotective.

XX OS Homo sapiens.

XX PN WO20016473-A2.

XX PD 25-MAY-2001.

XX PF 16-NOV-2000; 2000WO-US031581.

XX PR 16-NOV-1999; 99US-0165838P.

XX PR 17-NOV-1999; 99US-0166071P.

XX PR 19-NOV-1999; 99US-0166678P.

XX PR 28-DEC-1999; 99US-0173398P.

XX PR 22-FEB-2000; 2000US-0184124P.

XX PR 28-FEB-2000; 2000US-0185421P.

XX PR 02-MAR-2000; 2000US-0186653D.

XX PR 03-MAR-2000; 2000US-0186811P.

XX PR 09-MAR-2000; 2000US-0188114P.

XX PR 17-MAR-2000; 2000US-0190310P.

XX PR 21-MAR-2000; 2000US-0190800P.

XX PR 20-APR-2000; 2000US-0189569P.

XX PR 02-MAY-2000; 2000US-0201190P.

XX PR 08-MAY-2000; 2000US-0203111P.

XX PR 25-MAY-2000; 2000US-0207094P.

XX PI (PHAA) PHARMACIA & UPJOHN CO.

XX PI Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;

PI Schellin KA, Kaytes PS, Hannigan CM, Ruff V, Sejlitz T, Huff RM;
 XX WPI: 2001-389826/41.
 DR N-PSDB; AAH51008.
 XX PT New G protein-coupled receptor (GPCRx-x) and its encoding polynucleotide
 PT useful for diagnosing and treating e.g. schizophrenia.
 XX PS Claim 37; Page 89; 261pp; English.
 XX SQ The present invention relates to novel G protein-coupled receptors
 CC (nGPCRx), where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
 CC 31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
 CC one such G protein-coupled receptor. GPCRs are also known as seven
 CC transmembrane receptors and function in signal transduction. The nGPCRx
 CC coding sequences are useful for screening a human to diagnose a disorder
 CC affecting the brain or a genetic predisposition, specifically
 CC schizophrenia. nGPCRx are useful for identifying compounds useful for
 CC treating schizophrenia. Detection of nGPCRx in a sample is useful as a
 CC diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
 CC failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
 CC metabolic and cardiovascular disease, proliferative disorders and
 CC hormonal disorders. Modulators of nGPCRx activity have the utility for
 CC treating neurological disorders, including schizophrenia, ADHD/ADD
 CC (attention deficit-hyperactivity disorder, attention deficit disorder),
 CC and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
 CC migraine and senile dementia. Additional disorders include inflammatory
 CC conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
 CC disorders, cancers, respiratory ailments such as asthma, and inflammatory
 CC diseases e.g. inflammatory bowel disease
 XX Sequence 346 AA;
 - Query Match Score 1853; DB 4; Length 346;
 Best Local Similarity 100.0%; Pred. No. 7.4e-199;
 Matches 346; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1 MYNGSCCRIEGDTISQMPPLIVAFVIGALGENGVALGFCFPHMKTWKPTSTYLFNLAVAA 60
 Db 1 MYNGSCCRIEGDTISQMPPLIVAFVIGALGENGVALGFCFPHMKTWKPTSTYLFNLAVAA 60
 Qy 61 DFLMLICPFRDYKYLRRHWAFGDIPIRGVLFTLAMNTRAGSIVELTVADRYFKVHP 120
 Db 61 DFLMLICPFRDYKYLRRHWAFGDIPIRGVLFTLAMNTRAGSIVELTVADRYFKVHP 120
 Qy 121 HHAVENTISTRVAAGIVCWLTVLVLGTVLLENHLCVQETAVSCSFIMESANGWHIDM 180
 Db 121 HHAVENTISTRVAAGIVCWLTVLVLGTVLLENHLCVQETAVSCSFIMESANGWHIDM 180
 Qy 181 FOLEFFMPLGLILFCSPKIVWSLRROQLARORMKATRIMVALVFTCYLPVSAR 240
 Db 181 FQLEFFMPLGLILFCSPKIVWSLRROQLARORMKATRIMVALVFTCYLPVSAR 240
 Qy 241 LYPLWTVSSACDPVHGAHTLTSIYTMNSMLDPLIVYFSSSPPKPKYKLKICSLKPK 300
 Db 241 LYPLWTVSSACDPVHGAHTLTSIYTMNSMLDPLIVYFSSSPPKPKYKLKICSLKPK 300
 Qy 301 QPQHSKTKTQRPEMPISNIGRRCSTIVANSFQSOSGDQMDPHIVEWHD 346
 Db 301 QPQHSKTKTQRPEMPISNIGRRCSTIVANSFQSOSGDQMDPHIVEWHD 346

XX anabolic; cytostatic; antiviral; gene therapy; cardiomopathy; obesity;
 KW anorexia; diabetes; osteoporosis; Crohn's disease; multiple sclerosis;
 KW asthma; Alzheimer's disease; Parkinson's disorder; Huntington's disease;
 KW infection; human immunodeficiency virus; HIV.
 XX OS Homo sapiens.
 XX PN WO200174904-A2.
 XX PD 11-OCT-2001.
 XX PP 30-MAR-2001; 2001WO-US010241.
 PR 31-MAR-2000; 2000US-0193664P.
 PR 06-APR-2000; 2000US-0194614P.
 PR 06-APR-2000; 2000US-0195063P.
 PR 06-APR-2000; 2000US-0195066P.
 PR 06-APR-2000; 2000US-0195067P.
 PR 06-APR-2000; 2000US-0195068P.
 PR 06-APR-2000; 2000US-0195069P.
 PR 06-APR-2000; 2000US-0195070P.
 PR 06-APR-2000; 2000US-0195510P.
 PR 21-JUL-2000; 2000US-0219855P.
 PR 27-JUL-2000; 2000US-021984P.
 PR 28-JUL-2000; 2000US-02241325P.
 PR 11-AUG-2000; 2000US-0224488P.
 PR 11-AUG-2000; 2000US-0224488P.
 PR 18-JAN-2001; 2001US-0262508P.
 PR 23-JAN-2001; 2001US-026333P.
 PR 23-JAN-2001; 2001US-0263604P.
 PR 30-JAN-2001; 2001US-0265161P.
 PR 29-MAR-2001; 2001US-00823172.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Majunder K, Vernet CAM, Casman SJ, Wolenc AR, Spaderna SK;
 PI Padigaru M, Mishra VS, Tchernev VT, Spytek KA, Li L, Baumgartner JC;
 PI Gusev VY;
 XX DR WPI; 2001-639351/73.
 N-PSDB; ABA81529, ABA81530.
 XX PT New human G-protein coupled receptor X, GPCRX, polypeptide useful in
 PT treatment or prevention of GPCRX associated disorders e.g. cardiomopathy
 PT or atherosclerosis, and to screen for antagonists and agonists useful
 PT therapeutically.
 XX PS Claim 1; Page 8; 157pp; English.
 XX CC The invention relates to nucleic acid sequences (ABA81529-ABA81552) that
 CC encode G-coupled protein receptor related polypeptides (ABA44522-
 CC ABB44543). The isolated polypeptide having a sequence differing by no
 CC more than 15 % of amino acid residues from one of 22 amino acid sequences
 CC (or mature forms of the sequences), fully defined in the specification
 CC and corresponding to human G-protein coupled receptor X (GPCRX)
 CC polypeptides. The polypeptides have potential cardiotonic, antiarrhythmic,
 CC antihypertensive, antidiabetic, cytoprotective and antiviral activity. The
 CC polypeptides can be administered therapeutically, especially using gene
 CC therapy and expressing the encoding DNA in vivo, to treat or prevent
 CC GPCRX associated disorders, especially in humans. For example, they can
 CC be used to treat/prevent cardiomopathy, atherosclerosis, disorders
 CC related to signal processing and metabolic pathway modulation (e.g.
 CC obesity, anorexia), diabetes, osteoporosis, Crohn's disease, multiple
 CC sclerosis, asthma, cancers, neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Parkinson's disorder, Huntington's disease), immune disorders,
 CC haematopoietic disorders, developmental disorders, neurological disorders,
 CC bacterial, fungal, protozoal and viral infections (e.g. with human
 CC immunodeficiency virus (HIV-1 or HIV-2). They can be used diagnostically
 CC to determine the presence of or predisposition to a disease associated
 CC with altered levels of the polypeptide in mammals (especially humans) by
 CC detecting alterations in polypeptide expression levels relative to
 CC control samples. They are useful to identify agents binding polypeptide
 CC (e.g. cellular receptors or downstream effectors) and/or agents

CC modulating cellular polypeptide expression or activity, useful as
CC antagonists and agonists in disease treatment

XX Sequence 346 AA;
SQ Query Match 100.0%; Score 1853; DB 4; Length 346;
 Best Local Similarity 100.0%; Pred. No. 7.4e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC 1 MYNGSCCIEGDTISQMPPLIVAFVAGLNGVALGFCPHMKTWRPSTYLFNIAVA 60
 CC 1 MYNGSCCIEGDTISQMPPLIVAFVAGLNGVALGFCPHMKTWRPSTYLFNIAVA 60
 CC 61 DFLIMICLPERTDYLLRRHWAFGDIPCRVLFTLAMNRAGSTVFLTVAAADRYFKVWHP 120
 CC 61 DFLIMICLPERTDYLLRRHWAFGDIPCRVLFTLAMNRAGSTVFLTVAAADRYFKVWHP 120
 CC 121 HHAVENTISTRVAGIVCTWLAVLGTYLLENHLCVQETAVSCSFIMESANGHDIM 180
 CC 121 HHAVENTISTRVAGIVCTWLAVLGTYLLENHLCVQETAVSCSFIMESANGHDIM 180
 CC 181 FQLEFFMPMIGIILFCSFKIWSLRROQLARQRMKCATRIMVATFVITCYLPYSAR 240
 CC 181 FQLEFFMPMIGIILFCSFKIWSLRROQLARQRMKCATRIMVATFVITCYLPYSAR 240
 CC 241 LYFLWTVPSSACDPSPVHGALHTLSFTMNSMILDPLVYFSSSPSFPKYNKLKICSLKPK 300
 CC 241 LYFLWTVPSSACDPSPVHGALHTLSFTMNSMILDPLVYFSSSPSFPKYNKLKICSLKPK 300
 CC 301 QPGHSKTRQPRPEMPISNQGRSCTSVANSFQSOSDGDQDPHIVEWH 346
 CC 301 QPGHSKTRQPRPEMPISNQGRSCTSVANSFQSOSDGDQDPHIVEWH 346

RESULT 3

AAU06197
ID AAU06197 standard; protein; 346 AA.
XX
.AC AAU06197;

XX 19-DEC-2001 (first entry)
XX Novel human G protein-coupled receptor (GPCR) protein.
XX Human; G-protein coupled receptor; GPCR; chemokine receptor; protease;
KW hyperproliferative disorder; neurological disorder; psychiatric disease;
KW inflammatory disorder; respiratory disorder.
XX Homo sapiens.
OS WO200173029-A2.
XX 04-OCT-2001.
XX 27-MAR-2001; 2001WO-US009522.
XX PPF
XX 27-MAR-2000; 2000US-0192419P.
PR 06-SEP-2000; 2000US-0330459P.
PR 20-SEP-2000; 2000US-00666535.
XX (PEKE) PE CORP NY.

PI Ye J, Cravchik A, Di Francesco V, Beasley EM;
XX WPI; 2001-616503/71.
DR N-PSDB; AAS12581.

XX Novel human G-protein coupled receptor proteins and nucleic acid
PR molecules encoding the protein for use in developing human therapeutics
PR and diagnostic compositions and for identifying modulators of the
protein.
XX Claim 1; Fig 1; 66pp; English.

XX The present invention relates to the isolation of a novel human G-protein
CC coupled receptor (GPCR) which is related to the chemokine receptor
CC subfamily. The cDNA and gene sequences encoding for GPCR are also given
CC in the invention. The sequences of the invention are useful for
CC diagnosing and treating diseases or conditions mediated by human
CC proteases. Such diseases include hyperproliferative disorders (e.g.
CC hyperplasia), neurological disorders (e.g. Parkinson's disease),
CC psychiatric diseases (e.g. schizophrenia), inflammatory disorders (e.g.
CC diabetes) and respiratory disorders (e.g. adult respiratory distress
CC syndrome, ARDS). The GPCR protein is also useful for identifying a
CC modulator of the expression of the protein. It also serves as a target
CC for identifying agents for use in mammalian a therapeutic or pathological
CC e.g. a human drug, particularly modulating a biological or pathological
CC response in a cell or tissue that expresses the protein, in biological
CC assays related to GPCRs that are related to members of the chemokine
CC receptor subfamily, in drug screening assays and in competition binding
CC assays. GPCR is also useful in diagnosing a disease or predisposition to
CC a disease mediated by the peptide, in pharmacogenomic analysis. The
CC polynucleotide sequences can also be used in gene therapy. The present
CC sequence represents the novel human GPCR of the invention

XX SQ Sequence 346 AA;
SQ Query Match 100.0%; Score 1853; DB 4; Length 346;
 Best Local Similarity 100.0%; Pred. No. 7.4e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC 1 MYNGSCCIEGDTISQMPPLIVAFVAGLNGVALGFCPHMKTWRPSTYLFNIAVA 60
 CC 1 MYNGSCCIEGDTISQMPPLIVAFVAGLNGVALGFCPHMKTWRPSTYLFNIAVA 60
 CC 61 DFLIMICLPERTDYLLRRHWAFGDIPCRVLFTLAMNRAGSTVFLTVAAADRYFKVWHP 120
 CC 61 DFLIMICLPERTDYLLRRHWAFGDIPCRVLFTLAMNRAGSTVFLTVAAADRYFKVWHP 120
 CC 61 HHAVENTISTRVAGIVCTWLAVLGTYLLENHLCVQETAVSCSFIMESANGHDIM 180
 CC 61 HHAVENTISTRVAGIVCTWLAVLGTYLLENHLCVQETAVSCSFIMESANGHDIM 180
 CC 61 LYFLWTVPSSACDPSPVHGALHTLSFTMNSMILDPLVYFSSSPSFPKYNKLKICSLKPK 300
 CC 61 LYFLWTVPSSACDPSPVHGALHTLSFTMNSMILDPLVYFSSSPSFPKYNKLKICSLKPK 300
 CC 181 FOLEFFMPMIGIILFCSFKIWSLRROQLARQRMKCATRFIMVAVFLTCYLPYSAR 240
 CC 181 FOLEFFMPMIGIILFCSFKIWSLRROQLARQRMKCATRFIMVAVFLTCYLPYSAR 240
 CC 241 LYFLWTVPSSACDPSPVHGALHTLSFTMNSMILDPLVYFSSSPSFPKYNKLKICSLKPK 300
 CC 241 LYFLWTVPSSACDPSPVHGALHTLSFTMNSMILDPLVYFSSSPSFPKYNKLKICSLKPK 300
 CC 301 QPGHSKTRQPRPEMPISNQGRSCTSVANSFQSOSDGDQDPHIVEWH 346
 CC 301 QPGHSKTRQPRPEMPISNQGRSCTSVANSFQSOSDGDQDPHIVEWH 346

RESULT 4

AAU04373
ID AAU04373 standard; protein; 346 AA.

XX AAU04373;
XX AC
XX DT 23-OCT-2001 (first entry)
XX DE Human G-protein coupled receptor, hrUP19.
OS Homo sapiens.
XX KW Human; G-protein coupled receptor; GPCR; hrUP19; agonist;
KW inverse agonist; lung cancer.
XX OS Homo sapiens.
PN WO200136471-A2.

XX PR 25-MAY-2001.
PR 16-NOV-2000; 2000WO-US031509.

XX		Qy	301 QPGHSKTRQRPEMPISNLGRRSC1SVANSFQSOSITGQWDPHIVETH	346
PR	17-NOV-1999; 99US-0166088P.	Db	301 QPGHSKTRQRPEMPISNLGRRSC1SVANSFQSOSITGQWDPHIVETH	346
PR	17-NOV-1999; 99US-0166089P.			
PR	17-NOV-1999; 99US-0166369P.			
PR	23-DEC-1999; 99US-0171900P.			
PR	23-DEC-1999; 99US-0171901P.			
PR	23-DEC-1999; 99US-0171902P.			
PR	11-FEB-2000; 2000US-0181749P.			
PR	14-MAR-2000; 2000US-0188258P.			
PR	14-MAR-2000; 2000US-0189258P.			
PR	10-APR-2000; 2000US-0195898P.			
PR	10-APR-2000; 2000US-0195899P.			
PR	10-APR-2000; 2000US-0196078P.			
PR	28-APR-2000; 2000US-0200419P.			
PR	12-MAY-2000; 2000US-0203630P.			
PR	12-JUN-2000; 2000US-0210741P.			
PR	12-JUN-2000; 2000US-0210982P.			
PR	21-AUG-2000; 2000US-0195899P.			
PR	26-SEP-2000; 2000US-0226766P.			
PR	26-SEP-2000; 2000US-0235419P.			
PR	20-OCT-2000; 2000US-0242332P.			
PR	20-OCT-2000; 2000US-0242333P.			
PR	24-OCT-2000; 2000US-0243019P.			
XX	(AREN-) ARENA PHARM INC.			
PA				
PT	Chen R, Dang HT, Lowitz KP;			
XX				
DR	WPI: 2001-355616/37.			
DR	N-PSDB; AAS07946.			
XX				
PT	Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists, inverse agonists or partial agonists for use as therapeutic agents.			
PT				
PT	The sequence represents a human G-protein coupled receptor (GPCR), CC CCR19. The endogenous and non-endogenous, constitutively activated CC versions of human G-protein coupled receptors (GPCR), are useful for CC direct identification of candidate compounds as receptor agonists, CC inverse agonists or partial agonists having applicability as therapeutic CC agents for treating diseases related to GPCR, e.g. lung cancer. Non- CC endogenous version of human GPCRs are also utilized in research settings CC and in vitro and in vivo system, incorporating GPCRs can be utilized to CC elucidate and understand the roles these receptors play in the human CC condition, both normal and diseased.			
XX				
SQ	Sequence 346 AA;			
XX				
Query Match	1 MYNGSCCIEGDTISQMPPLLVAFVAGLNGVALGCPHMKTWKPSITYLFNIAVA 60			
Best Local Similarity	100.0%	Score	1853;	DB 4;
Matches	346;	Length	346;	
Conservative	0;	Mismatches	0;	Indels 0;
		Gaps	0;	
XX				
Qy	1 MYNGSCCIEGDTISQMPPLLVAFVAGLNGVALGCPHMKTWKPSITYLFNIAVA 60			
Db	1 MYNGSCCIEGDTISQMPPLLVAFVAGLNGVALGCPHMKTWKPSITYLFNIAVA 60			
Qy	61 DFLMICPFRDYIYLRRHWAFCDFPGRGLFTLAMNRAGS1VFLTVAAADRYFKVHP 120			
Db	61 DFLMICPFRDYIYLRRHWAFCDFPGRGLFTLAMNRAGS1VFLTVAAADRYFKVHP 120			
Qy	121 HHAVTISTRAVGIVCLWLAVLILGTYYLLENHLCYQETAVSCSFIMESANGHDIM 180			
Db	121 HHAVTISTRAVGIVCLWLAVLILGTYYLLENHLCYQETAVSCSFIMESANGHDIM 180			
Qy	181 FOLEFFMPGI1IIFCSPKIVWSRROQLQARMKCATRFMVAWFITCYLPSYSAR 240			
Db	181 FOLEFFMPGI1IIFCSPKIVWSRROQLQARMKCATRFMVAWFITCYLPSYSAR 240			
Qy	241 LYFLWTVPSACDPSVHGALHTLSFTMSMLDPLYTFMSLDPSSFPKYNKLKICSLKP 300			
Db	241 LYFLWTVPSACDPSVHGALHTLSFTMSMLDPLYTFMSLDPSSFPKYNKLKICSLKP 300			

myelofibrosis, psoriasis and cancer including adenocarcinoma, leukaemia, lymphoma; neurological disorders such as epilepsy, ischaemic cerebrovascular disease, Alzheimer's disease, Pick's disease, dementia, Parkinson's disease, ataxias, multiple sclerosis, bacterial and viral meningitis, Creutzfeld-Jakob disease, schizogenic disorders, amnesia; cardiovascular disorders such as arteriovenous fistula, atherosclerosis; hypertension, vascular tumours, myocardial infarction, hypertensive heart disease, infective endocarditis, myocarditis, myocardial ischaemia; gastrointestinal disorders such as dysphagia, peptic oesophagitis, emesis, anorexia, nausea, peptic ulcer, cholelithiasis, diarrhoea, constipation, acquired immune deficiency syndrome (AIDS), hepatic, encephalopathy; autoimmune/inflammatory disorders such as Addison's disease, allergies, spondylitis, amyloidosis, anaemia, asthma, contact dermatitis, Crohn's disease, diabetes mellitus, Goodpasture's syndrome, emphysema, Grave's disease, gout, multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus, uveitis, viral, bacterial, fungal, parasitic, protozoal and helminthic infections and trauma; and viral metabolic disorders such as diabetes, obesity and osteoporosis; and viral infections such as infection caused by viral agent classified as adenovirus, arenavirus, bunyavirus. Polynucleotides of the invention are useful as probes for assessing toxicity of test compounds. They are also used in gene therapy. The present sequence is human G-protein coupled receptor 3 (GCRC-3) protein.

Sequence 346 AA;

Query Match 100.0%; Score 1853; DB 5; Length 346;

Best Local Similarity 100.0%; Pred. No. 7.4e-199; Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCCIEGPDTSQNPPLLLIYAVIYFGALGNGVALGFCPAMKTKPSTVYLENLAVA 60

Db 1 MYNGSCCIEGPDTSQNPPLLLIYAVIYFGALGNGVALGFCPAMKTKPSTVYLENLAVA 60

Qy 61 DFLIMICLIPFRTDYLRLRRHWAEGDIPCRVGLFTLAMNRAGSIVELTVAAIRYFKVHP 120

Db 61 DFLIMICLIPFRTDYLRLRRHWAEGDIPCRVGLFTLAMNRAGSIVELTVAAIRYFKVHP 120

Qy 121 HHAVTNTISTRVAIGIVCLWLAWLIGTYLLENLHCVQETAVSCSFIMESANGHDIM 180

Db 121 HHAVTNTISTRVAIGIVCLWLAWLIGTYLLENLHCVQETAVSCSFIMESANGHDIM 180

Qy 181 PQLEFFMGLIILFCSPFLVLSRROQLQRQRMKATRFIMVAVFITYLPSVSR 240

Db 181 PQLEFFMGLIILFCSPFLVLSRROQLQRQRMKATRFIMVAVFITYLPSVSR 240

Qy 241 LYFLWTVSSACDPVSIGALHITSLTFSPTMSLDPLTYFSSSPFKYNYKLKICSLPK 300

Db 241 LYFLWTVSSACDPVSIGALHITSLTFSPTMSLDPLTYFSSSPFKYNYKLKICSLPK 300

Qy 301 QPCHKSKTRQEPEMPISNGGRSCTSVANSFQSOSDGDQDPHIVEWH 346

Db 301 QPCHKSKTRQEPEMPISNGGRSCTSVANSFQSOSDGDQDPHIVEWH 346

RESULT 6

ID AAU11401 standard; protein: 346 AA.

XX AAU11401;

XX DT 26-FEB-2002 (first entry)

XX DE HM74-like G-protein coupled receptor (GPCR).

XX HM74-like GPCR; G-protein coupled receptor; antibacterial; fungicide; protozoacide; analgesic; cyrostatic; neuroleptic; nootropic; anticonvulsant; tranquiliser; viral infection; pain; cancer; anoxia; bulimia; asthma; central nervous system disease; CNS disease; cardiovascular disease; hypertension; hypotension; angina pectoris; myocardial infarction; urinary retention; osteoporosis; ulcer; asthma; inflammation; allergy; benign prostatic hypertrophy; multiple sclerosis; psychiatric disorder; neurological disorder; dyskinesia;

KW Huntington's disease; Tourette's syndrome; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation.	
CC Homo sapiens.	
CC Key	Location/Qualifiers
CC Domain	/label= Transmembrane_domain_1
CC FT	20. .37
CC FT	/label= Transmembrane_domain_2
CC FT	.53. .73
CC FT	/label= Transmembrane_domain_3
CC Region	91. .113
CC FT	/label= Transmembrane_domain_4
CC FT	101. .118
CC FT	/label= GPCR_region
CC FT	/note= "G-protein coupled receptor region"
CC Domain	133. .150
CC FT	/label= Transmembrane_domain_5
CC Domain	180. .197
CC FT	/label= Transmembrane_domain_6
CC FT	223. .242
CC Domain	260. .279
CC FT	/label= Transmembrane_domain_7
CC XX	PN WO200177320-A2.
CC XX	XX 18-OCT-2001.
CC PD	XX 04-APR-2001; 2001WO-EP003811.
CC PR	XX 05-APR-2000; 2000US-0194701P.
CC PA	XX (FARB) BAYER AG.
CC XX	Xiao Y;
CC DR	XX WPI ; 2002-049147/06.
CC N-PSDB	DR AAS18501.
CC XX	XX Novel isolated polynucleotide, useful for treating infection, pain, cancer, asthma, hypertension, myocardial infarction, urinary retention, osteoporosis, encodes the human HM74-like G-protein coupled peptide.
CC XX	XX Claim 1; Fig 2; 77pp; English.
CC XX	The invention describes a novel isolated polynucleotide (I) encoding a human HM74-like G-protein coupled receptor (GPCR) polypeptide. Reagents that regulate HM74-like GPCR are useful for modulating the activity of the protein in a disease selected from bacterial, fungal, protozoan, and viral infection, pain, cancer, anoxia, bulimia, asthma, central nervous system (CNS) disease, cardiovascular disease, hypertension, angina pectoris, myocardial infarction, urinary retention, osteoporosis, ulcer, asthma, inflammation, allergy, benign prostatic hypertrophy, multiple sclerosis and dyskinesia such as Huntingon's disease and Tourette's syndrome. The composition is also useful for treating psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, delirium, dementia and severe mental retardation. (I) or the HM74-like GPCR polypeptide are also useful for treating the above mentioned diseases. (I) is useful in a diagnostic assay for detecting the presence of mutations in the nucleic acid sequences which encode a GPCR. The polypeptide is useful to identify test compounds which may act as agonists or antagonists at the receptor site and which can be regulated to provide therapeutic effects. The polypeptide is also useful as bait protein in a two-hybrid or three-hybrid assay, and to immunise a mammal for production of polyclonal antibodies. This is the amino acid sequence of human HM74-like GPCR described in the method of the invention.
CC SQ Sequence 346 AA;	SQ Sequence 346 AA;
CC SQ Best Local Similarity 100.0%; Pred. No. 7.4e-199;	CC Query Match 100.0%; Score 1853; DB 5; Length 346;

Page 6

AC ABB08596;
 XX DT 01-JUL-2002 (first entry)
 XX DS Human lipocyte-originated G protein-coupled receptor protein TGR13.
 XX KW Antiinflammatory; anorectic; obesity; inflammation; gene therapy; human;
 G protein-coupled receptor protein TGR13.
 XX OS Homo sapiens.
 XX PN WO200202767-A1.
 XX PD 10-JAN-2002.
 XX PF 02-JUL-2001; 2001WO-JP005711.
 XX PR 04-JUL-2000; 2000JP-00206860.
 PR 31-JUL-2000; 2000JP-00235274.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX PT Shibata S, Horikoshi K, Taniyama Y, Shintani Y, Miyajima N;
 XX DR WPI; 2002-164535/21.
 DR N-PSDB; ABA99236.
 XX PR New human lipocyte-originated G protein-coupled receptor proteins TGR13
 PR and encoding DNAs, for developing drugs to treat obesity and
 PR inflammations, including gene therapy.
 XX PS Claim 1; Fig 2; 101pp; Japanese.
 XX This invention relates to a human lipocyte-originated G protein-coupled
 receptor proteins TGR13, thought to be antiinflammatory and anorectic in
 their action. The proteins and encoded DNAs are for use in developing
 drugs to treat obesity and inflammation, including gene therapy. The
 present sequence represents the human lipocyte-originated G protein-
 coupled receptor protein TGR13.
 XX Sequence 346 AA;

Query	Match	Score 100.0%; Length 346;
	Best Local Similarity	100.0%; Pred. No. 7.4e-199;
	Matches	346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYNGSCCRLEGDTISQMPPLIYAFVGLGNGVALGFCFHMKTKPSTVYLFNLAVA 60
 DB 1 MYNGSCCRLEGDTISQMPPLIYAFVGLGNGVALGFCFHMKTKPSTVYLFNLAVA 60
 QY 61 DFLIMICLPRTDYLRRHWAEDIPCRVGLFTLAMTRAGSFTLVTAADRYFKVHP 120
 DB 61 DFLIMICLPRTDYLRRHWAEDIPCRVGLFTLAMTRAGSLVLTVAADRYFKVHP 120
 QY 121 HHAVNTISTRVAAGIVCWLALVLTGTYLLRNHLCYQETAVCSCESTIMESANGHDIM 180
 DB 121 HHAVNTISTRVAAGIVCWLALVLTGTYLLRNHLCYQETAVCSCESTIMESANGHDIM 180
 QY 181 POLEFFMPGIIILPCSFKIVWSLRRQQLARQARMKKTRFIMVATFITCYLPYSAR 240
 DB 181 POLEFFMPGIIILPCSFKIVWSLRRQQLARQARMKKTRFIMVATFITCYLPYSAR 240
 QY 241 LYFWMTVPSSACDPVSHGAHLHTISFTVNSMIDPLVYYFSSSPFKYVNKLKICSLRK 300
 DB 241 LYFWMTVPSSACDPVSHGAHLHTISFTVNSMIDPLVYYFSSSPFKYVNKLKICSLRK 300
 QY 301 QPGHSKTRQRPEEMPNISLGRCSRSCISVANSFOSQSDGQNDPHIVEWH 346
 DB 301 QPGHSKTRQRPEEMPNISLGRCSRSCISVANSFOSQSDGQNDPHIVEWH 346

Query Match Score 100.0%; Score 1853; DB 5; Length 346;
 Best Local Similarity 100.0%; Pred. No. 7.4e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MYNGSCCRLEGDTISQMPPLIYAFVGLGNGVALGFCFHMKTKPSTVYLFNLAVA 60

Sequence 346 AA;
 Query Match 100.0%; Score 1853; DB 5; Length 346;
 Best Local Similarity 100.0%; Pred. No. 7.4e-199;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MYNGSCCRLEGDTISQMPPLIYAFVGLGNGVALGFCFHMKTKPSTVYLFNLAVA 60

RESULT 14		Qy	181 FOLEFFMPLGILFCFSKIVASLRRQQLAROARMKKATRFIMVVAIVFTCYLPSYSRAR 240
ABP56751	DBP56751 standard; protein; 346 AA.	Db	181 FOLEFFMPLGILFCFSKIVASLRRQQLAROARMKKATRFIMVVAIVFTCYLPSYSRAR 240
XX		Qy	241 LYFLWTWTPSSACDPSPYSGALHITLSTTYMMNSMLDPLVYYFSSSPPKFYNLKICSLKPK 300
AC		Db	241 LYFLWTWTPSSACDPSPYSGALHITLSTTYMMNSMLDPLVYYFSSSPPKFYNLKICSLKPK 300
XX	31-MAR-2003 (first entry)	Qy	301 QPGHSKTRQRPEMPISNLGRSCISVANSFQSOSQDGWDPHIVEWH 346
XX	Human GAVE3 protein SEQ ID NO:2.	Db	301 QPGHSKTRQRPEMPISNLGRSCISVANSFQSOSQDGWDPHIVEWH 346
DE			
XX	KW Human; GAVE3; G protein-coupled receptor; GPCR; antiinflammatory; antiasthmatic; antirheumatic; antiarthritic; inflammatory disorder; asthma; chronic obstructive pulmonary disease; rheumatoid arthritis; chromosome 12.		
XX	OS Homo sapiens.		RESULT 15
XX	PN WO200300846-A2.	ID AAO26511 standard; protein; 346 AA.	
XX	PD 03-JAN-2003.	XX AAO26511;	
XX	PF 21-JUN-2002; 2002WO-US019430.	AC XX DT 13-FEB-2003 (first entry)	
XX	PR 22-JUN-2001; 2001US-00886041.	DE Human G-Protein Coupled Receptor protein.	
XX	DA (AVETIS PHARM INC.	XX KW Anorectic; antidiabetic; antiipaemic; antiasthmatic; antiinflammatory; antiallergic; antianginal; nephrotropic; hepatotropic; immunosuppressive; viricide; G-Protein agonist; G-Protein antagonist; dyslipidemia; G-Protein Coupled Receptor; obesity; diabetes; asthma; bronchitis; allergy; angina; glomerulonephritis; hepatitis; allograft rejection; human.	
XX	PI Xia T, Ni D, Eisinghrelo H, Ardati A, Minnich A, Jupp R;	XX KW	
XX	DR; 2003-184040/18.	OS Homo sapiens.	
XX	DR; AB222648.	XX PN WO200300846-A2.	
PT New GAVE3 nucleic acid and polypeptide, for preventing or treating a disorder associated with aberrant GAVE3 expression or activity, e.g. inflammatory disease, asthma, chronic obstructive pulmonary disease or rheumatoid arthritis.	XX PD 24-OCT-2002.	XX PI B Elliott SG, Rogers N, Busse LA;	
PT (AVETIS PHARM INC.	XX PF 14-FEB-2002; 2002WO-US004397.	XX PR 14-FEB-2001; 2001US-0269040P.	
XX	PS Claim 9; Fig 2; 90pp; English.	XX DR WPI; 2003-075524/07.	
XX	The present sequence represents a human G protein-coupled receptor (GPCR), designated GAVE3. GAVE3 is located on human chromosome 12. GAVE3 has antiinflammatory, antiasthmatic, antiarthritic, antiarthritic and antiarthritic activities. GAVE3 nucleic acids, polypeptides, agonists and antagonists can be used for preventing or treating a disorder associated with aberrant GAVE3 expression or activity, e.g. inflammatory disorders such as asthma, chronic obstructive pulmonary disease or rheumatoid arthritis. The nucleic acids and polypeptides can also be useful for identifying modulators, i.e. candidate or test compounds, that bind to GAVE3 proteins or have a stimulatory or inhibitory effect on GAVE3 expression or activity. The nucleotide sequences can also be used for chromosomal mapping, tissue typing or forensic biology. Root cells comprising GAVE3 can be used for producing non-human transgenic animals for studying the function and/or activity of GAVE3, or for identifying and/or evaluating modulators of GAVE3 activity.	XX DR N-PSDB; AU053846.	
XX	Sequence 346 AA;	XX PS Claim 13; Fig 1; 122pp; English.	
CC		XX CC The invention relates to a novel isolated G-Protein Coupled Receptor (GPCR) protein. The methods and compositions of the present invention are useful for diagnosis, treatment, amelioration and/or prevention of diseases associated with G-Protein Coupled Receptor (GPCR) polypeptides, such as obesity, diabetes, dyslipidemia, asthma, bronchitis, allergies, angina, glomerulonephritis, hepatitis, diabetes, asthma, allergies, angina and hepatitis.	
CC		XX CC PT New GPCR polypeptide and encoding nucleic acid molecule, useful for diagnosis, treatment and/or prevention of diseases associated with GPCR polypeptides, such as obesity, diabetes, asthma, allergies, angina and hepatitis.	
CC		XX CC Sequence 346 AA;	
CC		Query Match 100.0%; Score 1853; DB 6; Length 346; Best Local Similarity 100.0%; Pred. No. 7.4e-199; Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CC		Oy 1 MYNGSCCRIEGDTISQVMPLLLIVAFVQJALGNQVALGFCPEMKTWKPSVTYLENLA 60	
CC		Db 1 MYNGSCCRIEGDTISQVMPLLLIVAFVQJALGNQVALGFCPEMKTWKPSVTYLENLA 60	
CC		Db 61 DFLMICLCPFRTDYLRHRWAFGDIPIRGVLFTLAMNRAGSIVFTYVADRYFKVHP 120	
CC		Db 61 DFLMICLCPFRTDYLRHRWAFGDIPIRGVLFTLAMNRAGSIVFTYVADRYFKVHP 120	
CC		Oy 121 HHAVNTISTRVAAGIVCWLWVLTGTYLLENHLCYQTAVSCSESTIMESANGHDIM 180	
CC		Db 121 HHAVNTISTRVAAGIVCWLWVLTGTYLLENHLCYQTAVSCSESTIMESANGHDIM 180	
CC		Oy 61 DFLMICLCPFRTDYLRHRWAFGDIPIRGVLFTLAMNRAGSIVFTYVADRYFKVHP 120	

||||| 61 DFLMICPFRDYLLRHWAFGDI PORVGIFTLAMNRASSIVELTVAAADRYFKVWHP 120
Qy 121 HHAVENTISTRVAAGIVCTLWALVILGTYLLENHILCVOETAVSCSFIMESANGWHDIM 180
Db 121 HHAVENTISTRVAAGIVCTLWALVILGTYLLENHILCVOETAVSCSFIMESANGWHDIM 180
Qy 181 FOLEFFMPLGIIIFCSFKIVWSURRQOLARQARMKATRFIMVVAIVFTICLPSYSAR 240
Qy 181 FOLEFFMPLGIIIFCSFKIVWSURRQOLARQARMKATRFIMVVAIVFTICLPSVSAR 240
Db 181 LYFLWTVSSACDPSVHGALHTLSFTYMNMSLDPLVYFSSSPFPKPYNKLKICSLKP 300
Qy 241 LYFLWTVSSACDPSVHGALHTLSFTYMNMSLDPLVYFSSSPFPKPYNKLKICSLKP 300
Db 241 LYFLWTVSSACDPSVHGALHTLSFTYMNMSLDPLVYFSSSPFPKPYNKLKICSLKP 300
Qy 301 QPGHSKTRQPEEMPISNLGRRCSTIVANSFQSQSDGOWDPHIVEMH 346
Db 301 QPGHSKTRQPEEMPISNLGRRCSTIVANSFQSQSDGOWDPHIVEMH 346

Search completed: August 30, 2005, 18:30:49
Job time : 169 secs

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;ID: S33733
 R;Webb, T.E.; Simon, J.; Krishke, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock
 PEBS Lett. 324, 219-225, 1993
 A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
 A;Reference number: S33733; MUID:93285340; PMID:8508924
 A;Accession: S33733
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-362 <WEB>
 A;Cross-references: UNIPROT:P34996; EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:93950
 C;Superfamily: ATP receptor P2u
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.68; Score 364; DB 2; Length 362;
 Best Local Similarity 29.1%; Pred. No. 9.5e-26;
 Matches 95; Conservative 58; Mismatches 130; Indels 44; Gaps 7;

Qy 18 MPPLIVAFVULGNGVALCGFCFMKTKWPKSTVLFNLAVADFLMILCPFRTDYLR 77
 Db 43 LPTVYLIVFITEFLGNSVATINNEFEVHPRWSCLSYMVNLALADFYVUTPALLFYFFEN 102
 Qy 78 RRHWAFGDPICRVLGLTETLAMNRGGTIVELTVAAIRYSGVYPLMSLGRKKRNAYVIS 173
 Db 103 KTDWIFGDVMCKLQRFPHVNLYSILETLCISVHRTGVTHPLSLGRKKRNAYVSS 162
 Qy 138 TLWALVLTGTYLLENHLCVQET-AVSC-----ESFIMESANGWHDIMFQLEFFM 187
 Db 174 LWLWVVGSPILYSGTGTGKRNKTRITCYDTSDBYLRSYISM-----CTVAMFCV 228

RESULT 4
 JC4737
 G protein-coupled receptor P2Y1 - human
 G;Protein-coupled receptor P2Y1 - human
 G;Alternative names: P2Y1 purinergic receptor; P2Y1 purinoceptor
 C;Species: Homo sapiens (man)
 C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
 C;Accession: JC4737; JC4615; 554253
 R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
 Biochem. Biophys. Res. Commun. 221, 588-593, 1996
 A;Title: Cloning and tissue distribution of the human P2Y1 receptor.
 A;Reference number: JC4737; MUID:96205320; PMID:9630005
 A;Accession: JC4737
 A;Molecule type: DNA
 A;Residues: 1-373 <DNAN>
 A;Cross-references: UNIPROT:P47900; GB:S81950; NID:g1839438; PIDN:AAA47091.1; PID:g18394
 R;Ayyanathan, R.; Webb, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P.
 Biochem. Biophys. Res. Commun. 218, 783-788, 1996
 A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
 A;Accession: JC4615
 A;Molecule type: mRNA
 A;Residues: 1-373 <AY>
 A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
 R;Henderson, D.J.; Elliott, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
 Biochem. Biophys. Res. Commun. 212, 648-656, 1995
 A;Title: Cloning and characterisation of a bovine P2Y receptor.
 A;Reference number: JC4162; MUID:95352058; PMID:7626079
 A;Accession: JC4162
 A;Molecule type: mRNA
 A;Residues: 1-373 <HEN>
 A;Cross-references: UNIPROT:P48042; EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:9103
 A;Experimental source: aortic endothelial cell
 C;Genetics:

RESULT 3
 JC4162
 P2Y receptor - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Accession: JC4162
 C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 R;Henderson, D.J.; Elliott, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
 Biochem. Biophys. Res. Commun. 212, 648-656, 1995
 A;Title: Cloning and characterisation of a bovine P2Y receptor.
 A;Reference number: JC4162; MUID:95352058; PMID:7626079
 A;Accession: JC4162
 A;Molecule type: mRNA
 A;Residues: 1-373 <HEN>
 A;Cross-references: UNIPROT:P48042; EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:9103
 A;Gene: bovP2Y
 C;Superfamily: ATP receptor P2u
 C;Keywords: Glycoprotein; phosphoprotein; receptor; transmembrane protein
 C;Genetics:
 F;52-77/Domain: transmembrane #status predicted <TM1>
 F;78-111/Domain: transmembrane #status predicted <TM2>
 F;124-150/Domain: transmembrane #status predicted <TM3>
 F;171-191/Domain: transmembrane #status predicted <TM4>
 F;214-237/Domain: transmembrane #status predicted <TM5>
 F;261-282/Domain: transmembrane #status predicted <TM6>
 F;305-328/Domain: transmembrane #status predicted <TM7>
 F;88-111/Domain: transmembrane #status predicted <TM2>
 F;124-150/Domain: transmembrane #status predicted <TM3>
 F;171-191/Domain: transmembrane #status predicted <TM4>
 F;214-237/Domain: transmembrane #status predicted <TM5>

Query Match 19.68; Score 362.5; DB 2; Length 373;

intron 17 purinergic receptor P2Y5 - human N;Alternate names: G-protein coupled receptor C;Species: Homo sapiens (man) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T09508 R;Author, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W. A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinoblastoma gene. It is a member of the G-protein coupled receptor family. A;Reference number: Z16705 A;Accession: T09508 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-344 <BoH> A;Cross-references: UNIPROT:P43657; EMBL:AF000546; NID:92232068; PID:92232069 C;Genetics: C;Superfamily: ATP receptor P2u C;Keywords: G protein-coupled receptor; transmembrane protein	Qy 124 VNTISTRVAAGIVCTIWLAVLYVLTGTVYLLENHLCYOETAVSCES----- Db 142 LRWGGRARYARRVAAVWVLVLAQCPVLYVTTSRGTRITCHDTSARELFSHFTAYSS- Qy 175 GHWDIMFQLEFFMPGIIILCSCKTWSLRRQQ-----LARQARMKKATRPMVVA 226 Db 201 ---WMLGLLFAVPEPSVILYC---YVLMARLLKPAYGRTGGLPRAKR--KSVRTALVL 251 Qy 227 IVPITCYLP-SVSARLYPLMTVPSACDP--SVHGHALHTTSFTYNSMLDPLVYFSSP 283 Db 252 AVFALCFLPHVTRLYYSRSLSDDSCHTNAINNAYKTRPLASANSCLDPVLFPLAQ 311 Qy 284 SFPKYNKLKICSLKPKOEGHSIKTOR 309 Db 312 RLVRFARDAK----PTEPTPSQAR 333
RESULT 9	
A;Cross-references: UNIPROT:P47749; EMBL:U09632; NID:9495197; PID:AAA18498.1; PID:g4951	
Query Match 151667	
Best Local Similarity 30.8%; Conservative 56%; Mismatches 120; Indels 22; Gaps 10;	Species: Xenopus laevis (African clawed frog) C;Species: Xenopus laevis (African clawed frog) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 C;Accession: T09508 R;Gerzten, R.B.; Chen, J.; Ishii, M.; Nanovicz, T.; Turck, C.M.; Vu, T.H.; C;Nature: 368, 648-651, 1994 A;Title: Thrombin receptor's specificity for agonist peptide is determined by its extracellular domain A;Reference number: 151667; PMID:94195429; PMID:8145852 A;Accession: 151667 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-420 <BoH> A;Cross-references: UNIPROT:P47749; EMBL:U09632; NID:9495197; PID:AAA18498.1; PID:g4951
Matches 88; Conservative 56; Mismatches 133; Indels 37; Gaps 10;	Query Match Score 310.5; DB 2; Length 420; Best Local Similarity 28.0%; Pred. No. 9.3e-21; Matches 88; Conservative 56; Mismatches 133; Indels 37; Gaps 10;
Qy 24 VAFVLGALGNQVALCGPFCHMKTKWPSTVYLENLAVADDELMICLPERTDYLLRRHHWAP 83 Db 26 MYFVLGIVNSNCVAYIYIFCVLRNEETTYMINLANSDDLLVEFTLPERI-TYFTTENWPP 84	Qy 14 ISQVNMPPLLIVAFVLGALGNQVALCGPFCHMKTKWPSTVYLENLAVADELLMICLPERTD 73 Db 100 LTKFPLSYTTFVIGPLPLNLIAITFLFKMKVRPAVVMNLNLADAVPEFSVLPFKIA 159
Qy 84 GDITPCRVQLFLTLMANRAGSIVFELTVVADRYFKVHPHAVTNTISTRVAAGIVCTI-WMAL 142 Db 85 GDLICKSIVMLFYTNMYGSIILEFTCISVDRFLAIVYPPKS-KTLRKTKRANKAVCTGWLT 143	Qy 74 YLRLRRHWAEGDIPCRVGFLFTLAMNRAGSIVFELTVVADRYFKVHPHAVTNTISTRVA 133 Db 160 YHLSGNDWLFPGMCRIVTALEYCNMCSVLLIASISVDFRLAVVYPMHSUSW-RTMRA 218
Qy 143 VLTGT---VYLLLENHLCYQETAVSCESFIMESANGWHIMFOL-----EFFMPGIIIL 193 Db 144 VIGGSAPPAVFVQOTHQNNNASACFEMFPEAT--WKLTYLIVITFIVFPIULAV 201	Qy 134 GIVCL-LWALVLTGTVYLL---ENHLCVQETAVSCESFI-MESANGWHIMFQ---LEF 185 Db 219 YMACSFPLWLIASITPLVLTQTKIPRLDITTCVDLKDLDKFYIYFSSFLUFF 278
- Qy 194 FCSFKTWSLRRQQQLARQARMK-KATRPMVVAIVPITCYLP-SVSARLYPL--WTVP 248 Db 202 TCSSMVVLTQLTKPTVLSRSKINKTKVLMIFVHLIFCFCPYNTNLILYSLVRLQTFLV 261	Qy 186 FMPGLGILPFSFKTWSLRRQQQLARQARMKKATRPMVVAIVFITC-----YL 234 Db 279 FVPFRITTCYTGIRSL-SSSIINSCKETRALIAVVVLCVFTICFGPTNVLFTHYL 337
Qy 249 SSACDPSVYRGALHITLSEFTYMSMLDPLVYVYSSSPSPKFPYNNKLKI 294 Db 262 NCSSVVAAVRTMYPITLCAVSNCCFDPVIYVYFTSDT--IONSIKRM 304	Qy 235 PSVSLARLYPLMTVPSAACDPSVYRGALHITLSEFTYMSMLDPLVYVSSSPSPKFPYNNKLKI 294 Db 338 QEANFVYFAVL-----SCCUDPLVYASSQORYVYSL-L 381
RESULT 8	
A47556 ATP receptor P2u - mouse C;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004 C;Accession: A47556 R;Justiz, K.D.; Shiao, A.K.; Brake, A.J.; Julius, D. Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993 A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells. A;Reference number: A47556; PMID:93281707; PMID:7655114 A;Accession: A47556 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-373 <BoH> A;Cross-references: UNIPROT:P35383; GB:L14751; NID:9309457; PID:9309458 C;Superfamily: ATP receptor P2u C;Keywords: transmembrane protein	Qy 295 CSLKPQKGHSKTO 308 Db 382 CCRVSEPGSSTGQ 395
Best Local Similarity 30.1%; Pred. No. 1.1e-21; Matches 98; Conservative 44; Mismatches 150; Indels 34; Gaps 8;	RESULT 10 157940 somatostatin receptor 5 - rat N;Alternate names: somatotropin release-inhibiting factor subtype 28 receptor C;Species: Rattus norvegicus (Norway rat) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004 C;Accession: 157940; 157949; 539244 R;O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C. Mol. Pharmacol. 42, 939-946, 1992 A;Title: Molecular cloning and expression of a pituitary somatostatin receptor with pre-

A; Reference number: 157940; MUID:93125499; PMID:1367243	C; Keywords: G protein-coupled receptor; hormone receptor; transmembrane protein
A; Accession: 157940	Query Match 16.6%; Score 307; DB 2; Length 391;
A; Status: preliminary; translated from GB/EMBL/DBJ	Best Local Similarity 25.7%; Pred. No. 1.8e-20;
A; Molecule type: mRNA	Matches 85; Conservative 62; Mismatches 130; Indels 54; Gaps 9;
A; Residues: 1-363 <OCA1>	
A; Cross-references: UNIPROT:P30398; GB:L04535; NID:9409238; PIDN:AAA17029.1; PID:9409239	Qy 4 GSCCRTEGD-----TISQMPPLVIIIVFV-----LGALGNGVALCGF 40
R; O'Carroll, A.M.; Loiait, S.J.; Konig, M.; Mahan, I.C.	Db 24 GACSGEGSGAAGMBEPGRNASONGTLSEGGSSAILSFYSSVCLNLCONSMVYIYI 83
Mol. Pharmacol. 44, 1278, 1993	
A; Title: Molecular cloning and expression of a pituitary somatostatin receptor with pre	
A; Accession: 157949	Qy 41 CFHMKTWKPSVTYFLNLFADFLMLCPLPFTDYLRRHAFGDPICRVLGLFTLAMRNRA 100
A; Status: preliminary; translated from GB/EMBL/DBJ	Db 84 LRYAKMTATNTYIYLNAIADEMLMSVPFLVTSU-LRHWPFGALICRLVLSVDAVNMF 142
A; Molecule type: mRNA	
A; Residues: 341-363 <OCA2>	
A; Cross-references: GB:S67370; NID:9455947; PIDN:AAE29371.1; PID:9455948	Qy 101 GSIVFLTVVAADRYFKVVPHEANTISTRVAGIVCTLWALVIGTIVLLLENHLCV-Q 159
A; Experimental source: Pituitary	Db 143 TSIYCLTVLSVDRYAVVHPPIKAARYRPTVAKVNVLGWVWLILPVIVFSRTAANS 202
R; Penetta, R.; Greenwood, M.; Patel, Y.C.	
Submitted to the EMBL Data Library, August 1993	
A; Description: Correction of the nucleotide and amino acid sequence of the rat somatosta	
A; Reference number: S39244	Qy 160 ETAVSCSFIMESANGWHD---IMPFOLFFMPLGITLFC-----SFKIVWSLR 204
A; Accession: S39244	Db 203 DTRVACNMLMPPPAQRLVGFVLYTFMLGFLPVGAIICLVLYLIAKRMVYALKGWQR 262
A; Molecule type: mRNA	
A; Residues: 309-363 <OPEN>	Qy 205 RRQLARQARMKKATRIMVVAIFITCYLPVSARLYFLMTVPSAACDPSVHGALHITL 264
A; Cross-references: EMBL:X74828; NID:9433311; PIDN:CAA52825.1; PID:9433912	Db 263 KRSE-----RKITLMVMMTYMVFTICWMMPFYVQLVNVAEQQDDAT-----VSQLSV 309
C; Genetics:	
A; Gene: SSR5	Qy 265 SFTYNNENLDPHLVYFESSPSFBPKPYNKLKIC 295
C; Superfamily: vertebrate rhodopsin	Db 310 ILGYANSCANPILYGFLLSDNFNRKFQSFORI-LC 339
Query Match 16.7%; Score 309.5; DB 2; Length 363;	RESULT 12
Best Local Similarity 29.6%; Pred. No. 9.8e-21;	A1795
Matches 96; Conservative 53; Mismatches 148; Indels 27; Gaps 9;	somatostatin receptor 1 - human
	Species: Homo sapiens (man)
	C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
	C; Accession: A41795
	R; Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
	Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
	A; Title: Cloning and functional characterization of a family of human and mouse somatost
	A; Reference number: A41795; MUID:92108031; PMID:1346068
	A; Molecule type: DNA
	A; Residues: 1-391 <YAM>
	A; Cross-references: UNIPROT:P30872; GB:MB1829; NID:9307433; PIDN:AAAS8247.1; PID:9307434
	A; Note: sequence extracted from NCBI backbone (NCBIN:74767, NCBI:74768)
	A; Gene: GDB:SSTR1
	A; Cross-references: GDB:134185; OMIM:182451
	A; Map position: 14q12-14q13
	A; Introns: #status absent
	C; Superfamily: vertebrate rhodopsin
	C; Key words: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; phc
	F; 58-84/Domain: transmembrane #status predicted <TM1>
	P; 95-120/Domain: transmembrane #status predicted <TM2>
	F; 132-153/Domain: transmembrane #status predicted <TM3>
	F; 173-195/Domain: transmembrane #status predicted <TM4>
	F; 220-250/Domain: transmembrane #status predicted <TM5>
	F; 269-296/Domain: transmembrane #status predicted <TM6>
	F; 302-326/Domain: transmembrane #status predicted <TM7>
	F; 44,44,381/Binding site: carbohydrate (Asn) (covalent) #status predicted
	F; 130-208/Disulfide bonds: #status predicted
	F; 172/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predicted
	F; 265/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
	F; 339/Binding site: palmitate (Cys) (covalent) #status predicted
Query Match 16.5%; Score 305.5; DB 2; Length 391;	RESULT 11
Best Local Similarity 26.3%; Pred. No. 2.5e-20;	C41795
Matches 81; Conservative 62; Mismatches 128; Indels 37; Gaps 8;	somatostatin receptor 1 - mouse
	C; Species: Mus musculus (house mouse)
	C; Date: 30-Sep-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
	C; Accession: C41795
	R; Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.
	Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992
	A; Title: Cloning and functional characterization of a family of human and mouse somatosta
	A; Reference number: A41795; MUID:92108031; PMID:1346068
	A; Accession: C41795
	A; Status: nucleic acid sequence not shown
	A; Molecule type: DNA
	A; Residues: 1-391 <YAM>
	A; Cross-references: UNIPROT:P30873; GB:MB1831; NID:9201058; PIDN:AAAS8255.1; PID:9201059
	C; Superfamily: vertebrate rhodopsin
Query Match 10 EGDSQMPPLVIAFV-----LGALGNGVALCGFCEFMKTCWPKSTVLFNLAYADFL 63	Db 47 QNSTLSEQQGSAILSFYSSVCLGLCGNSMVIYVILRYAKMTATNIYILNLADEL 106

Qy	64	LMICLPPPTDYYLRRHWAEGDIPCRVGLFTLAMNRAGSIVELTVAAADRYFKVYHPHHA	123	Db	279	VFVICMPPEYVQVLNVFAEQDDAT-----VSQSVLGYANSANCANPILYGELSDFNFKR	332
Db	107	LMLSVPFVFTSTL-LRHPPGAUCLCRVLSDAVNMFSTYCLTVLSVDRTAVAVHPKA	165	Qy	288	FYNKLKIC	295
Qy	124	VNTISTRVAAAGIVCTLWALVILGTYVLLLENHLCV-QETAVSCESFIMESANGWHD---	178	Db	333	SFQRI-LC	339
Db	166	ARYRRTPTAKVNLGVWVSLSLVLPIVFSRSTAANSDTGTAVCNMNMPEPAQRWLWGFVL	225				
RESULT 14							
Qy	179	IMFQLEFFPMGLGILFC-----SFKIVWSLRROQLAROARMKKATRFIMVAI	227				
Db	226	YTFELMGFLPVGAICLYCVLIIAKMRMVAALKAGWQRKRSR-----RKITLMVMVM	278				
Qy	228	VFTTCYLPSVSARSLYFLMTVPSSACDPSVHGALHITLSTFTYNSMILDPLVYFSSPSFPK	287				
Db	279	VFVICMPPEYVQVLNVFAEQDDAT-----VSQSVLGYANSANCANPILYGELSDFNFKR	332				
Qy	288	FYNKLKIC	295				
Db	333	SFQRI-LC	339				
RESULT 15							
A39297							
somatostatin receptor - rat G-protein-coupled receptor; SRIF receptor							
N:Alternate names: probable G-protein-coupled receptor; SRIF receptor							
C:Species: <i>Rattus norvegicus</i> (Norway rat)							
C:Date: 03-Aug-1992 #Sequence_revision 03-Aug-1992 #text_change 09-Jul-2004							
R:Meyerhof, W.; Paust, H.J.; Schoenrock, C.; Richter, D.							
DNA Cell Biol. 10, 685-694, 1991.							
A:Title: Cloning of a cDNA encoding a novel putative G-protein-coupled receptor expressed in brain.							
A:Reference number: A39297, MUID:92096119, PMID:1661599							
A:Accession: A39297							
A: Molecule type: mRNA							
-A:Residues: 1-391 <MEX>							
A:Cross-references: UNIPROT:P28846; GB:X62314; GB:Y61630; NID:956309; PIDN:CAA44193.1; F							
A:Experimental source: brain							
A:Note: it is uncertain whether Met-1 is the initiator or whether translation is initiated at residue 2.							
R,Li, X.J.; Force, M.; North, R.A.; Ross, C.A.; Snyder, S.H.							
J. Biol. Chem. 267, 21303-21312, 1992							
A:Title: Cloning and expression of a rat somatostatin receptor enriched in brain.							
A:Reference number: A5102; MUID:93016064; PMID:1400442							
A:Status: preliminary; not compared with conceptual translation							
A:Molecule type: nucleic acid							
A:Residues: 1-391 <L11>							
A:Experimental source: brain							
A:Note: sequence extracted from NCBI backbone (NCBIP:116692)							
C:Superfamily: vertebrate rhodopsin							
C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein							
Query Match 16.5% Score 305.5 DB 2 Length 391;							
Best Local Similarity 26.3% Pred. No. 2, 5e-20; Matches 81; Conservative 62; Mismatches 128; Indels 37; Gaps 8;							
RESULT 15							
B41795							
somatostatin receptor 2 - human							
C:Species: <i>Homo sapiens</i> (man)							
C:Date: 31-Dec-1993 #Sequence_revision 31-Dec-1993 #text_change 09-Jul-2004							
C:Accession: B41795							
R:Yamada, Y.; Post, S.R.; Wang, K.; Tager, H.S.; Bell, G.I.; Seino, S.							
Proc. Natl. Acad. Sci. U.S.A. 89, 251-255, 1992							
A:Title: Cloning and functional characterization of a family of human and mouse somatost							
A:Reference number: A41795; MUID:92108031; PMID:1346068							
A:Molecule type: DNA							
A:Residues: 1-369 <YAM>							
A:Cross-references: UNIPROT:P20874; GB:W61830; NID:9307435; PIDN:AAA58248.1; NCBI:74770							
C:Genetics;							
A:Gene: SSTR2							
A:Cross-references: GDB:134186; OMIM:182452							
A:Map position: 17q24-17q24							
Qy	10	EGDTISQMPPLIIVAFV-----IGAIGNGVALCGFCEHHMKTKWPSTVYLFLNLAVALDFL	63	Db	47	QNCTLSECGSALLISFYSSVVLGLGNSMVIYVILYARMKTAATNYTINLADEL	106
Db	64	LMICLPPPTDYYLRRHWAEGDIPCRVGLFTLAMNRAGSIVELTVAAADRYFKVYHPHHA	123	Qy	124	VNTISTRVAAAGIVCTLWALVILGTYVLLLENHLCV-QETAVSCESFIMESANGWHD---	178
Db	107	LMLSVPFVFTSTL-LRHPPGAUCLCRVLSDAVNMFSTYCLTVLSVDRTAVAVHPKA	165	Db	166	ARYRRTPTAKVNLGVWVSLSLVLPIVFSRSTAANSDTGTAVCNMNMPEPAQRWLWGFVL	225
Qy	124	VNTISTRVAAAGIVCTLWALVILGTYVLLLENHLCV-QETAVSCESFIMESANGWHD---	178	Qy	179	IMFQLEFFPMGLGILFC-----SFKIVWSLRROQLAROARMKKATRFIMVAI	227
Db	166	ARYRRTPTAKVNLGVWVSLSLVLPIVFSRSTAANSDTGTAVCNMNMPEPAQRWLWGFVL	225	Qy	179	IMFQLEFFPMGLGILFC-----SFKIVWSLRROQLAROARMKKATRFIMVAI	227
Db	226	YTFELMGFLPVGAICLYCVLIIAKMRMVAALKAGWQRKRSR-----RKITLMVMVM	278	Db	228	VFVICMPPEYVQVLNVFAEQDDAT-----VSQSVLGYANSANCANPILYGELSDFNFKR	332
Qy							

A; Introns: #status absent
 C; Superfamily: vertebrate rhodopsin
 C; Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pho
 F; 44-69 /Domain: transmembrane #status predicted <TM1>
 F; 80-105 /Domain: transmembrane #status predicted <TM2>
 F; 117-138 /Domain: transmembrane #status predicted <TM3>
 F; 158-180 /Domain: transmembrane #status predicted <TM4>
 F; 205-235 /Domain: transmembrane #status predicted <TM5>
 F; 254-281 /Domain: transmembrane #status predicted <TM6>
 F; 288-315 /Domain: transmembrane #status predicted <TM7>
 F; 9, 22, 29, 32, 351/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F; 115-193/Disulfide bonds: #status predicted
 F; 250/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted
 F; 328/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match Score 302.5; DB 2; Length 369;
 Best Local Similarity 29.8%; Pred. No. 4.4e-20;
 Matches 90; Conservative 50; Mismatches 135; Indels 27; Gaps 9;

Qy	13 TISQVMPULLIAFVLGALGNVALCGFCFAMKTKWPSTVILENLAVADFLLMICLPPRT 72
Db	41 TSNAVLTPIFYVVCILIGICGNTLIVYVILRVAKMKTITNITYLNLATADELFLMLGLPFLA 100
Qy	73 DYLRRRHWAEGDIPCRGLFTLAMNRAGSIVELTVVAADRYFKWVPHHAINTISTRVA 132
Db	101 -MQVALVHWWPFGKAICRVMVMTDGINQFTSIFCLTVMNSIDRYLAVVHPPIKSAKWRPRTA 159
Qy	133 AGIVCTIWA--LIVLG-TVYLLENHLCVQETAVSCESFIMESANGWHD---IMFOLE 184
Db	160 KNTIMAWGVSLIVLPLMIYAGLRSN--QMGRSSCTINPGESEGAWTGFLIYTFLIG 216
Qy	185 FFMPLGILFCFSKIVWSLR---RROQLQARMKKATRPMVMAVPICTYLPVSAR 240
Db	217 FLYPLTICLCLVLFILIKVKSSGIRVSSSKRKSEKKVTRMSIVVAFIFCWLP---- 271
Qy	241 LYFLWTVSSAC---DPSVHGALHITLSFTYMSMILDPLVYFSSSPFPKYNKULKICS 296
Db	272 -FVIFNVSSVSMASISPTEPALIKGMDFVVLTYANSACMPIYAFSLSDNPKGSFQNV-LCL 329
Qy	297 LK 298
Db	330 VK 331

Search completed: August 30, 2005, 18:34:36
 Job time : 44 secs

THIS PAGE BLANK (USPTO)

Result No.	Score	Query Match	Length	DB ID	Description
1	881.5	47.6	387	4	US-09-170-496D-222 Sequence 222, App
2	880.5	47.5	387	4	US-09-170-496D-108 Sequence 108, App
3	880.5	47.5	387	4	US-09-944-807-21 Sequence 21, App
4	529	28.5	423	2	US-08-955-713-2 Sequence 2, App
5	510	27.5	476	2	US-08-955-713-4 Sequence 4, App
6	451.5	24.4	319	3	US-09-130-749-2 Sequence 2, App
7	451.5	24.4	319	3	US-09-130-749-2 Sequence 4, App
8	448.5	24.2	319	4	US-09-170-496D-60 Sequence 60, App
9	448.5	24.2	319	4	US-09-170-496D-196 Sequence 196, App
10	371	20.0	362	3	US-08-513-974B-374 Sequence 374, App
11	362.5	19.6	373	2	US-08-559-524A-4 Sequence 4, App
12	362.5	19.6	373	3	US-08-749-707-4 Sequence 4, App
13	362.5	19.6	373	4	US-09-942-922-4 Sequence 6, App
14	361.5	19.5	346	4	US-09-585-876-2 Sequence 2, App
15	354	19.1	373	4	US-09-745-842-14 Sequence 14, App
16	346.5	18.7	370	3	US-08-781-250-2 Sequence 2, App
17	336	18.1	339	1	US-08-153-848-44 Sequence 44, App
18	336	18.1	339	2	US-08-812-871-3 Sequence 3, App
19	335	18.1	339	3	US-09-299-843A-44 Sequence 44, App
20	335	18.1	339	3	US-09-088-337B-44 Sequence 44, App
21	336	18.1	339	4	US-09-170-496D-32 Sequence 32, App
22	335	18.1	339	5	PCT-US93-11153-44 Sequence 44, App
23	335	18.1	339	5	PCT-US95-07180-2 Sequence 2, App
24	335	18.1	339	4	US-09-170-496D-182 Sequence 182, App
25	328.5	17.7	302	2	US-08-467-948A-30 Sequence 30, App
26	328.5	17.7	302	3	US-08-467-947A-30 Sequence 30, App
27	327	17.6	309	3	US-09-422-869-20 Sequence 20, App

RESULT 2
 US-09-170-496D-108
 Sequence 108, Application US/09170496D
 Patent No. 6553339
 GENERAL INFORMATION:
 APPLICANT: Behan, Dominic P.
 APPLICANT: Chalmers, Derek T.
 APPLICANT: Liaw, Chen W.
 TITLE OF INVENTION: No. 6553339-Endogenous, Constitutively Activated Human G Protein-Software, PatentIn version 3.1
 FILE REFERENCE: AREN-0040
 CURRENT APPLICATION NUMBER: US/09/170,496D
 CURRENT FILING DATE: 1998-10-13
 NUMBER OF SEQ ID NOS: 294
 SEQ ID NO: 108
 LENGTH: 387
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-170-496D-108

Query Match 47.5%; Score 880.5; DB 4; Length 387;
 Best Local Similarity 52.2%; Pred. No. 6.1e-68;
 Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;

Qy 5 SCCRIEGDTISQMPPLIVAVFLGALGNQEVALCGPCFMKTKWPSVYLNLAVIDFLL 64
 Db 17 NCCVFRDDFLAKVLPVLGEFFGLLNGNLWPCFHLSKWSRFLNLAVIDFLL 76

Qy 65 MCLPFDTYLRRHWAFGDIPCRVGLFTLAMNRAGSIVELTVAAADRYFKVPHPHAV 124
 Db 77 TICLPPFDYTYRSRDSWNFGDIPCRVLFLMFAMNRQSSIFLTWVAVDRYFRVPHHAL 136

Qy 125 NTISTRVAAGIVCTWLALVIGTYYLLENHLCVQETAVSCSFIMESANGWHDIMFQL 184
 Db 137 NKISNWTAIIISCLLWGITGLTVHLKKLJONGPANCISFSCHTPRWEAMFLE 196

Qy 185 FMPMLGLILFCFSKIVWSLRQOLARQAMRKATRFTMVAIVFITYCLPVSARLYFL 244
 Db 197 PLLPGILFCFSARIISLQR-QMDRAKTRFTMVAIVFITYCLPVSARLYFL 255

Qy 245 WTPSSA---CD--PSVHGALHITLSPYTMNSMLDPVYFFFSSPKFYKNKLKICSLKP 299
 Db 256 WLHTSGTQNCEVRSVDAFFITLSPYTMNSMLDPVYFFFSSPKFYKNKLKICSLKP 315

RESULT 4
 US-08-955-713-2
 Sequence 2, Application US/08955713
 Patent No. 5955308
 GENERAL INFORMATION:
 APPLICANT: SATHE, GANESH
 APPLICANT: MOONEY, JEFFREY
 APPLICANT: BERGSM, DERK
 APPLICANT: HALSEY, WENDY
 TITLE OF INVENTION: CDNA CLONE HE0AD54 THAT ENCODES NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 STREET: P.O. BOX 980
 CITY: VALLEY FORGE
 STATE: PA
 COUNTRY: USA
 ZIP: 19482
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/955,713
 FILING DATE: 23-OCT-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION NUMBER: 60/050,124
 APPLICATION NUMBER: 60/050,124
 FILING DATE: 18-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: PRESTIA, PAUL F
 REGISTRATION NUMBER: 23,031
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: GH-70087
 TELEPHONE: 610-407-0700
 TELEX: 846169
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 423 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

RESULT 3
 US-09-944-807-21
 Sequence 21, Application US/09944807
 Patent No. 6773895
 GENERAL INFORMATION:
 APPLICANT: Boehringer Ingelheim Pharma KG
 TITLE OF INVENTION: Method for identifying substances which positively influence inflammatory conditions of chronic inflammatory airway diseases
 FILE REFERENCE: 082_00n
 CURRENT APPLICATION NUMBER: US/09/944,807
 CURRENT FILING DATE: 2001-05-31
 PRIOR APPLICATION NUMBER: UK 0021484.1
 PRIOR FILING DATE: 2000-09-01
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 21
 LENGTH: 387
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-944-807-21

Query Match 47.5%; Score 880.5; DB 4; Length 387;

US-08-955-713-2

Query Match	28.5%	Score 529; DB 2; Length 423;
Best Local Similarity	39.2%	Pred. No. 1.1e-37;
Matches	115; Conservative	48; Mismatches 108; Indels 22; Gaps 7;
Qy	4 GSCCRIBEDTISOMPPMPLIVAFVGLAUGNGVALGFPHMKTWKPSTVYLENLAVALDFL 63	
Db	81 GPCHPTSSVLVSAAFLAPILAEFLVGLGNSSLALPFLHTREWTNTVFLSVAADF 140	
Qy	64 LMICLPLFTDYLRLRRAJGDPGDIPCRVLGFLTLMNRAGCIVPLTVVADRYFKVWHPHHA 123	
Db	141 LISNLPLDVYDYLHLHTRGAACKVNLFMLSTMNRPAVVELTAAIARVLYKVKQPHHV 200	
Qy	124 VNTISTRVYAGIVCTLWAVLVLTGVYLLLENHLICVQB-TAVSCSEFSIM---ESANGWHD 178	
Db	201 LSRAVGAAARVAGGLWGI-----LWLNGHILLSTSFGPSCLSYRVGKTESASLRWMHQ 254	
Qy	179 IMFOQLEFFMPGLTILFCFSKIVWSLRRQOQLARQARMKKATRFIMVVAIVFITYLPSV- 237	
Db	255 ALVLEFLPLALLFLFAVSGIITRN-GLGQQAGPGRAMEVLYAMVAVYTICFLPSII 313	
Qy	238 --SARLYFLWTPVSSA--CDPSVHGALHITLSTFTYNNMSIDPLVYYFSSPSF 285	
Db	314 FGNASMYAFWLSACRSLLDCTQLFHG---SLAFTYLNVSVDPLVYCFSSPNF 362	

RESULT 5

US-08-955-713-4

Sequence 4, Application US/08555713
Patent No. 5955308
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: MOONEY, JEFFREY
APPLICANT: BERGMA, DERK
APPLICANT: HALSYN, WENDY
TITLE OF INVENTION: cDNA CLONE HE0AD54 THAT ENCODES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSSEE: RATTNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,713
FILING DATE: 23-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,124
FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE DOCKET NUMBER: GH-70087
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

RESULT 6

US-09-130-749-2

Sequence 2, Application US/09130749
Patent No. 601090
GENERAL INFORMATION:
APPLICANT: SHABON, USMAN ELSHOURBAGY, NABIL
TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATTNER & PRESTIA
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
COMPILER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,749
FILING DATE: 07-AUG-1998
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UNKNOWN
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE DOCKET NUMBER: GP-70513
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-130-749-2

Query Match 24.4%; Score 451.5; DB 3; Length 319;
 Best Local Similarity 34.4%; Pred. No. 3.8e-11;
 Matches 101; Conservative 61; Mismatches 121; Indels 11; Gaps 5;

Qy 7 CRIEGDTISQMPPLIVAVTVALGNGVALCGFCFIMKTPSTYFLNIAVADFLIMI 66
 Db 6 CSAPSTVATAVGVNLGLECGGLGLGNAGNAVALWTFRVRVKPVAVLLNLADILLAA 65

Qy 67 CLPFRTDYLRRHAWFGDPCRVGLFTLAMRAGSIVELTVADRYFKVPHPAVNT 126
 Db 66 CLPFLAAYFLSLQAHGLGRVCCWALRFELLSRSVGMAGFLAAVALDRYLRVHPRKVN 125

Qy 127 ISTRVAGIVTCLWLVLGTVLLENHLCVQETAVSCSFIMESANG----WHDIMF 181
 Db 126 LSPQAALGVSGLWLMVAUTCPGLLSE--AAQNSTRCHSF-YSRADGSFSIIWOBALS 182

Qy 182 QLEFFMPPLGILFCSPKIVNSLRRR-QQLARQARMKKATRIMVVAIFTCYLPVSAR 240
 Db 183 CLQFVLPFGLVFCNAGITRALQKLREPEPKQPKLORAQALVTLVFLALCFLPCLFLAR 242

Qy 241 -LYFIMTVSSACDPSVGAHLHTISFTMNSMDPLVTVFSSSPPKFYTNKL 292
 Db 243 VLMHIFQNLGSRCRALCAVAHTSDVTGSLTYLHSVNPVVYCFSSPTFRSSYRRV 296

Db 243 VLMHIFQNLGSRCRALCAVAHTSDVTGSLTYLHSVNPVVYCFSSPTFRSSYRRV 296

RESULT 8
 US-09-170-496D-60
 ; Sequence 60, Application US/09170496D
 ; Patient No. 6555339
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P.
 ; CHAMBERS: Chameris, Derek T.
 ; ATTORNEY: Liaw, Chen W.
 ; TITLE OF INVENTION: Constitutively Activated Human G Protein-
 ; TITLE OF INVENTION: Receptors
 ; FILE REFERENCE: AREN-0040
 ; CURRENT APPLICATION NUMBER: US/09/170,496D
 ; CURRENT FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 294
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 60
 ; LENGTH: 319
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-170-496D-60

Query Match 24.2%; Score 448.5; DB 4; Length 319;
 Best Local Similarity 34.0%; Pred. No. 6.9e-31;
 Matches 100; Conservative 62; Mismatches 121; Indels 11; Gaps 5;

Qy 7 CRIEGDTISQMPPLIVAVTVALGNGVALCGFCFIMKTPSTYFLNIAVADFLIMI 66
 Db 6 CSAPSTVATAVGVNLGLECGGLGLGNAGNAVALWTFRVRVKPVAVLLNLADILLAA 65

Qy 67 CLPFRTDYLRRHAWFGDPCRVGLFTLAMRAGSIVELTVADRYFKVPHPAVNT 126
 Db 66 CLPFLAAYFLSLQAHGLGRVCCWALRFELLSRSVGMAGFLAAVALDRYLRVHPRKVN 125

Qy 127 ISTRVAGIVTCLWLVLGTVLLENHLCVQETAVSCSFIMESANG----WHDIMF 181
 Db 126 LSPQAALGVSGLWLMVAUTCPGLLSE--AAQNSTRCHSF-YSRADGSFSIIWOBALS 182

Qy 182 QLEFFMPPLGILFCSPKIVNSLRRR-QQLARQARMKKATRIMVVAIFTCYLPVSAR 240
 Db 183 CLQFVLPFGLVFCNAGITRALQKLREPEPKQPKLORAQALVTLVFLALCFLPCLFLAR 242

Qy 241 -LYFIMTVSSACDPSVGAHLHTISFTMNSMDPLVTVFSSSPPKFYTNKL 292
 Db 243 VLMHIFQNLGSRCRALCAVAHTSDVTGSLTYLHSVNPVVYCFSSPTFRSSYRRV 296

RESULT 9
 US-09-170-496D-196
 ; Sequence 196, Application US/09170496D
 ; Patent No. 6555339

Query Match 24.4%; Score 451.5; DB 3; Length 319;
 Best Local Similarity 34.4%; Pred. No. 3.8e-31;

GENERAL INFORMATION:

APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.

TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-Receptors

CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 196
LENGTH: 319
TYPE: PRT
ORGANISM: Homo sapiens

US-09-170-496D-196

Query Match 24.2%; Score 448.5; DB 4; Length 319;
Best Local Similarity 34.0%; Pred. No. 6.9e-31; Indels 11; Gaps 5;
Matches 100; Conservative 62; Mismatches 121;

Qy 7 CRLGDTISQWMPPLITAVFLGALGNQVALCGFCFMKTKWPSTVYENLAVADEPILMI 66
Db 6 CSAPSTVVATAVGGVLLGIECGUGLGNNAVALWTFELFRVWNPAYVLLNLALADLILAA 65

Qy 67 CLPFRTDYLRRHWAFLFEDIPCRVGLFTFLAMNRAGSIVFLTVVAADDYFKVWHPHHAINT 126
Db 66 CLFLAAATYLSLOAHLRGRGVCAFLRFLDLSAVGMFLAVALDYLRLRVHPRLKVNLL 125

Qy 127 ISTRVAAGIVCTILWALVLTGTYLLENHLCVQETAVCESFTIMESANG----WHIDMF 181
Db 126 LSPQAALGVSGLYWLLMVALTCPEGLLSE--AAQNSTRCHSP-YSRADGSFSIWIQELS 182

Qy 182 QLERFPMPGIIIFLCFSKIVWSLRR--QOLARQARMKATRFIMVAVTFITCYLPVSAR 240
Db 183 CLOQVLPGLIVFCNAGIRALQKRLEPEKPKLQRKAALKLVVVVFLCFLPCFLAR 242

Qy 241 --LYFLWTVPSACDPSTYHGALHITLSFTYNSMLDPLIYVYFSSSPSPKFYNKL 292
Db 243 VLMHIFQNLGSCRALCAVAHTSDVTGSLITYLHSVVNPVYCFSSPTFRSSYRRV 296

RESULT 10
US-08-513-974B-374
Sequence 374, Application US/08513974B

GENERAL INFORMATION:
Patent No. 6114139

APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Fukusumi, Tetsuya
APPLICANT: Ohgi, Kazuhiro

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380

CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513, 974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

Db 327 ATRKSSRSEP-NVQSSSEEMTLNL 351

RESULT 12
US-08-749-707-4
; Sequence 4, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REFERENCE/DOCKET NUMBER: 044481-5010-00-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-749-707-4

Query Match 19 6%; Score 362.5; DB 3; Length 373;
Best Local Similarity 27.5%; Pred. No. 2e-23; Mismatches 68; Indels 140; Gaps 7;
Matches 92; Conservative 68; MisMatches 68; NMatches 140; Indels 35; Gaps 7;

Qy 18 MPPLIVAVPVLGAUNGVALCGCFAMTKWPKSTVYLENLAVALDFMLICLPRTDYLR 77
Db 54 LPAVYLVIFIGLNSVATWMEFTMKPWSGISYMMENALADFLYVLTPLALIFYFN 113
Qy 78 RRHWAFGDIPCRVGIFTLMNRAGSIVFLTYVAADRYFKVWHHAVTISTRVAGIVC 137
Db 114 KDWIFGDAMCKLQRFLPHVNLYGSILFLTCISAHYSGVVPLKSLSRLKCKNAVYISV 173
Qy 138 TIWAVLVLGTUYLLNHLCVQET-AVSC-----ESTIMEANGWHIDMPQEFFF 187
Db 174 LWVAVVGGSPILYSGTGIRKNTITCYDTSDEYLRSFYISM-----CTTVAMFCV 228
Qy 188 PLGILFCSFKIVWSLRQQLAROARNKATRFIMVAIVITCYLP-----ESFIMESANGWHIDMPQEFFF 187
Db 174 LYFLIVVYGISPLIFYSGTGIRKNTITCYDTSDEYLRSFYISM-----CTTVAMFCV 228
Db 229 PLVILGCGYLIVRALIYK-DLDNSPLRKSIYLIVLTVFAVSYTPHMKTMLR 287
Qy 188 PLGILFCSFKIVWSLRQQLAROARNKATRFIMVAIVITCYLP-----SVSAR 240
Db 241 LYFLWTVPSACDPYVGHALHTISPTYNSMIDLPIVYFSSPSFPKFYNKLKICSLKPK 300
Qy 241 LYFLWTVPSACDPYVGHALHTISPTYNSMIDLPIVYFSSPSFPKFYNKLKICSLKPK 300
Db 288 LDF-QTPEMCAFNDRVATYQVTRGLASLNCSVDPILFLAGDTFRRLSR----- 337
Qy 301 QPGHSKTKTORPEMPSNLGRCSISVANSFQSQSD 335
Db 338 -ATRKA3RSEANLQSKESEDMTILNLSBFKQNGD 370

RESULT 13
US-09-947-922-4

Sequence 4, Application US/09947922
 Patent No. 6680373
 GENERAL INFORMATION:
 APPLICANT: Conley, Pamela B.
 INVENTOR: Jantzen, Hans-Michael
 TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: MORGAN, LEWIS & ROCKIUS LLP
 STREET: 1800 M Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20036-5869
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/947,922
 FILING DATE: 07-SEP-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/749,707
 ATTORNEY/AGENT INFORMATION:
 NAME: Adler, Reid G.
 FILING DATE: 15-NOV-1996
 REGISTRATION NUMBER: 30,988
 REFERENCE/DOCKET NUMBER: 044481-5010-01-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-467-7000
 TELEFAX: 202-467-7176
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 373 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPology: linear
 MOLECULE TYPE: protein
 SEQ DESCRIPTION: SEQ ID NO: 4:
 US-09-947-922-4

Query Match 1.8 MPPLILAVFLGALGNQVALCFCFHMKTKWPKSTVYLNLAVDFLMICLPLFRDYLR 77
 Best Local Similarity 27.5%; Prod. No. 2e-23; Length 373;
 Matches 68; Mismatches 140; Indels 35; Gaps 7;

Db 54 LPavyILVFLIGLGNSVIAWWFMHCKPWSGISVYMFNLALLDFLYLTLPALIYFN 113

Qy 78 RRHWAFGDIPCRVGLFTLAMNTRAGSIVLTVVADRYKPVVPHHAINTTISTRVAAGJVC 137
 Db 114 KTDWIFGDMCKLQRFLPFLVNLGSILUPLTCISAHRVSGVYPLKSLGRKKKNVYTSV 173

Qy 138 TVALVLIQTVLLENLHCQET-----ESFTIMESANGWHDIMEQLEFFM 187
 Db 174 LMLIVVNGISPLIFYSGTGIRKNTKTTCYDTSDEVIRSYFYSM-----CTTVAMFCV 228

Qy 188 PLGILIFCSFKIYWSLRLRQQQLARQARMKKATRFIMVVAIVFTCYLP-----SVAR 240
 Db 229 PLVLIGCYGLIVRALIYK-DLDNSPLRKSTVILVITLVPAVSYTFHVNKTMNLR 287

Qy 241 LYFWMTVSSACBDSVHGHITLSFTMSMDPLVYFSSPSFPKEYNKLKICSLKP 300
 Db 288 LDF-QTPMCNAFDRVAYTQVTRGLASINSVCDPFLYFLAGDTFRRLSR----- 337

Qy 301 QPGHSIKTSKPIISNLRGRSCLVANSFQSQSD 335
 Db 338 -ATRKASRSEANLQSSEDMTNILSEPKQNGD 370

RESULT 14

Qy 78 RRHWAFGDIPCRVGLFTLAMNTRAGSIVLTVVADRYKPVVPHHAINTTISTRVAAGJVC 137
 Db 114 KTDWIFGDMCKLQRFLPFLVNLGSILUPLTCISAHRVSGVYPLKSLGRKKKNVYTSV 173

Qy 138 TVALVLIQTVLLENLHCQET-----ESFTIMESANGWHDIMEQLEFFM 187
 Db 174 LMLIVVNGISPLIFYSGTGIRKNTKTTCYDTSDEVIRSYFYSM-----CTTVAMFCV 228

Qy 188 PLGILIFCSFKIYWSLRLRQQQLARQARMKKATRFIMVVAIVFTCYLP-----SVAR 240
 Db 229 PLVLIGCYGLIVRALIYK-DLDNSPLRKSTVILVITLVPAVSYTFHVNKTMNLR 287

Qy 241 LYFWMTVSSACBDSVHGHITLSFTMSMDPLVYFSSPSFPKEYNKLKICSLKP 300
 Db 288 LDF-QTPMCNAFDRVAYTQVTRGLASINSVCDPFLYFLAGDTFRRLSR----- 337

Qy 301 QPGHSIKTSKPIISNLRGRSCLVANSFQSQSD 335
 Db 338 -ATRKASRSEANLQSSEDMTNILSEPKQNGD 370

RESULT 15

Qy 78 RRHWAFGDIPCRVGLFTLAMNTRAGSIVLTVVADRYKPVVPHHAINTTISTRVAAGJVC 137
 Db 114 KTDWIFGDMCKLQRFLPFLVNLGSILUPLTCISAHRVSGVYPLKSLGRKKKNVYTSV 173

Qy 138 TVALVLIQTVLLENLHCQET-----ESFTIMESANGWHDIMEQLEFFM 187
 Db 174 LMLIVVNGISPLIFYSGTGIRKNTKTTCYDTSDEVIRSYFYSM-----CTTVAMFCV 228

Qy 188 PLGILIFCSFKIYWSLRLRQQQLARQARMKKATRFIMVVAIVFTCYLP-----SVAR 240
 Db 229 PLVLIGCYGLIVRALIYK-DLDNSPLRKSTVILVITLVPAVSYTFHVNKTMNLR 287

Qy 241 LYFWMTVSSACBDSVHGHITLSFTMSMDPLVYFSSPSFPKEYNKLKICSLKP 300
 Db 288 LDF-QTPMCNAFDRVAYTQVTRGLASINSVCDPFLYFLAGDTFRRLSR----- 337

Qy 301 QPGHSIKTSKPIISNLRGRSCLVANSFQSQSD 335
 Db 338 -ATRKASRSEANLQSSEDMTNILSEPKQNGD 370

RESULT 14

; FEATURE INFORMATION: P2Y1 purinergic receptor; p2yr
 ; OTHER INFORMATION: P2Y1 purinergic receptor; p2yr
 US-09-745-842-14

Query Match Similarity 19.1%; Score 354; DB 4; Length 373;
 Best Local Similarity 29.2%; Pred. No. 1_1e-22;
 Matches 93; Conservative 66; Mismatches 132; Indels 28; Gaps 8;
 Matches 93; Mismatches 132; Indels 28; Gaps 8;

Qy 18 MPPMLIIVAFVIGALGNGVALCGFCPHMKTWKESTKVLFLNLAVADELIMICLPLFRTDYLRL 77
 Db 54 LPAVVILVIFIIGFLGNVAIWWFVNPKWGSISYMFNLALADFLYVLTIPALIFYFN 113
 Qy 78 RRHWAEGDIPCRVGLPTLMNRAGSIVLTVAAADRYFKVYHPHAINTISTRVAAGIVC 137
 Db 114 KTDWIFSDAMCKLQRFPHNLYGSILFLTCUARHGSGVYPLKSURAKKONICISV 173
 Qy 138 TLWALVLTGTVYLLNLHQET-AVSC-----ESFIMESANGWDIMFOLEFFM 187
 Db 174 LWLIVVVAISPLIFYSGTGEVKNKTTCYDTSDEYLRSFIYSM----CTTVAMFCV 228
 Qy 188 PGLLILPCESEKLYWSLERRQQLARQAEKKATREIIMVAVITCYLP-----SVSAR 240
 Db 229 PLVFLIGCYGLIVRALIYK-DLDNSPARKSYLTVLVTYFAVSTIPHYMKTINLRAR 287
 Qy 241 LYFLWTVSSACDPSVHGALHTLSFTYMSHLDPVYFSSSPKFKYNKLKICSLKPK 300
 Db 288 LDF-QTPAMCAFNDRYVATYQVTRGLASINSCTVDPFLYLAQDTPR--RLSRATRKAS 343
 Qy 301 QPGHSIKTO-RPEEPMISNL 318
 Db 344 RRSEANLQSKSEDMTLNIL 362

Search completed: August 30, 2005, 18:35:23
 Job time : 45 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2005 18:28:13 ; Search time 162 Seconds
 (without alignments)
 839.213 Million cell updates/sec

Title: US-10-719-692-6

Perfect score: 1853

Sequence: 1 MYNGSCRCIEGDTISQVNPP.....ANSFQSQSDGQNDPHIVEWH 346

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/_ptodata/1/pubcaa/US07_PUBCOMB.pep:*

2: /cgn2_6/_ptodata/1/_pubcaa/FCT_NEW_PUB.pep:*

3: /cgn2_6/_ptodata/1/_pubcaa/US06_NEW_PUB.pep:*

4: /cgn2_6/_ptodata/1/_pubcaa/US06_PUBCOMB.pep:*

5: /cgn2_6/_ptodata/1/_pubcaa/BCTUS_PUBCOMB.pep:*

6: /cgn2_6/_ptodata/1/_pubcaa/US07_NEW_PUB.pep:*

7: /cgn2_6/_ptodata/1/_pubcaa/US08_NEW_PUB.pep:*

8: /cgn2_6/_ptodata/1/_pubcaa/US08_PUBCOMB.pep:*

9: /cgn2_6/_ptodata/1/_pubcaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/_ptodata/1/_pubcaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/_ptodata/1/_pubcaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/_ptodata/1/_pubcaa/US09_NEW_PUB.pep:*

13: /cgn2_6/_ptodata/1/_pubcaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/_ptodata/1/_pubcaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/_ptodata/1/_pubcaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/_ptodata/1/_pubcaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/_ptodata/1/_pubcaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/_ptodata/1/_pubcaa/US10 NEW_PUB.pep:*

19: /cgn2_6/_ptodata/1/_pubcaa/US11A_PUBCOMB.pep:*

20: /cgn2_6/_ptodata/1/_pubcaa/US11 NEW_PUB.pep:*

21: /cgn2_6/_ptodata/1/_pubcaa/US60 NEW_PUB.pep:*

22: /cgn2_6/_ptodata/1/_pubcaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1853	100.0	346	9	US-09-867-274-2
2	1853	100.0	346	9	US-09-942-374-2
3	1853	100.0	346	10	US-09-988-01-2
4	1853	100.0	346	10	US-09-974C-80
5	1853	100.0	346	14	US-10-188-149A-2
6	1853	100.0	346	14	US-10-019-384-18
7	1853	100.0	346	14	US-10-200-842-2
8	1853	100.0	346	14	US-10-225-567A-668
9	1853	100.0	346	14	US-10-201-481-7
10	1853	100.0	346	14	US-10-278-141-3
11	1853	100.0	346	14	US-10-322-807-24

ALIGNMENTS

RESULT 1
 US-09-862-274-2
 ; Sequence 2, Application US/09862274
 ; Patent No. US20020052022A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ELSHOORBAGY, NABIL
 ; APPLICANT: GATTU, MAHANAND BESHWAR
 ; APPLICANT: SHABON, USMAN
 ; APPLICANT: IGNAR, DIANE MICHELE
 ; TITLE OF INVENTION: MOLECULAR CLONING OF A CHEMOKINE LIKE
 ; TITLE OF INVENTION: 7MTR (AXOR87)
 ; FILE REFERENCE: GP-70703-1
 ; CURRENT APPLICATION NUMBER: US/09/862,274
 ; CURRENT FILING DATE: 2001-05-22
 ; PRIOR APPLICATION NUMBER: US 09/580,675
 ; PRIOR FILING DATE: 2000-05-30
 ; PRIOR APPLICATION NUMBER: GB 0026839.1
 ; PRIOR FILING DATE: 2000-11-02
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 346
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 ; US-09-862-274-2

Query Match Similarity 100.0%; Score 1853; DB 9; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.6e-163;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCRCIEGDTISQVNPPLLIVAVTGAINGNGALCGFCFHMTKWPSTVLYLFLAVA 60
 Db 1 MYNGSCRCIEGDTISQVNPPLLIVAVTGAINGNGALCGFCFHMTKWPSTVLYLFLAVA 60

RESULT 3
 US-09-886-041-2
 ; Sequence 2, Application US/09886041
 ; Patent No. US20030059869A1
 ; GENERAL INFORMATION:
 ; APPLICANT: XIA, TAI-HB
 ; APPLICANT: NI, DONGRUI
 ; APPLICANT: BISHENGDELO, HAIFENG
 ; APPLICANT: ARDITI, ALI
 ; APPLICANT: MINNICH, ANNE
 ; APPLICANT: JUPP, RAY
 ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR
 ; FILE REFERENCE: 41491
 ; CURRENT APPLICATION NUMBER: US/09/886,041.
 ; CURRENT FILING DATE: 2003-06-22
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 346
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-886-041-2

Query 61 DFLMICLPCFRTDYLLRRHAWFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 Db 61 DFLMICLPCFRTDYLLRRHAWFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 Qy 121 HHAVENTISTRVAAGIVCTWLAVLIGTYLQENHLICVQETAVSCSFIMESANGWHDIM 180
 Db 121 HHAVENTISTRVAAGIVCTWLAVLIGTYLQENHLICVQETAVSCSFIMESANGWHDIM 180
 Qy 181 FOLEFFMGLILFCSPKIVWSLRRQOLQARMKTRFIMVAIVFTICLPSVAR 240
 Db 181 FOLEFFMGLILFCSPKIVWSLRRQOLQARMKTRFIMVAIVFTICLPSVAR 240
 Qy 241 LYFLWTVSSACDPSVGAHLITSLFVYFSSPSPKFYNLKICSLKPK 300
 Db 241 LYFLWTVSSACDPSVGAHLITSLFVYFSSPSPKFYNLKICSLKPK 300
 Qy 301 QPGHSKTRQRPEEMPSNIGRRCISVANSFQSOSQGDGWDPHIVEMH 346
 Db 301 QPGHSKTRQRPEEMPSNIGRRCISVANSFQSOSQGDGWDPHIVEMH 346

RESULT 2
 US-09-942-374-2
 ; Sequence 2, Application US/09942374
 ; Patent No. US20020137063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gluckmann, Maria Alexandra
 ; APPLICANT: Gimeno, Ruth
 ; APPLICANT: White, David
 ; TITLE OF INVENTION: 57242, a Human G-Protein Coupled Receptor Family Member and Uses Therefor
 ; FILE REFERENCE: MP120000-368PBR
 ; CURRENT APPLICATION NUMBER: US/09/942,374
 ; CURRENT FILING DATE: 2001-08-29
 ; PRIOR APPLICATION NUMBER: US 60/228,409
 ; PRIOR FILING DATE: 2000-08-29
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 2
 ; LENGTH: 346
 ; TYPE: PRT
 ; ORGANISM: human
 ; US-09-942-374-2

Query Match 100.0%; Score 1853; DB 10; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.6e-163; Mismatches 0; Indels 0; Gaps 0;
 Matches 346; Conservative 0; N mismatches 0; Delins 0; Gaps 0;

Qy 1 MYNGSCCIEGDTISQWMPPLIVAFVQLGNGVALCGPROFHMKTWKPSVYLNLAVA 60
 Db 1 MYNGSCCIEGDTISQWMPPLIVAFVQLGNGVALCGCFHMKTWKPSVYLNLAVA 60
 Qy 61 DFLMICLPCFRTDYLLRRHAWFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 Db 61 DFLMICLPCFRTDYLLRRHAWFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 Qy 121 HHAVNTISTRVAAGIVCTWLAVLIGTYLQENHLICVQETAVSCSFIMESANGWHDIM 180
 Db 121 HHAVNTISTRVAAGIVCTWLAVLIGTYLQENHLICVQETAVSCSFIMESANGWHDIM 180
 Qy 181 FQLEFFMPLGILFCSPKIVWSLRRQOLQARMKTRFIMVAIVFTICLPSVAR 240
 Db 181 FQLEFFMPLGILFCSPKIVWSLRRQOLQARMKTRFIMVAIVFTICLPSVAR 240
 Qy 241 LYFLWTVSSACDPSVGAHLITSLFVYFSSPSPKFYNLKICSLKPK 300
 Db 241 LYFLWTVSSACDPSVGAHLITSLFVYFSSPSPKFYNLKICSLKPK 300
 Qy 301 QPGHSKTRQRPEEMPSNIGRRCISVANSFQSOSQGDGWDPHIVEMH 346
 Db 301 QPGHSKTRQRPEEMPSNIGRRCISVANSFQSOSQGDGWDPHIVEMH 346

RESULT 4
 US-09-782-974C-80
 ; Sequence 80, Application US/09782974C
 ; Publication No. US20030082534A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vogeli, Gabriel
 ; APPLICANT: Lind, Peter
 ; APPLICANT: Wood, Linda S.
 ; APPLICANT: Paredi, Luis A.
 ; TITLE OF INVENTION: No. US-0030082534A1 e G Protein Coupled Receptor
 ; FILE REFERENCE: 411USPHRM311
 ; CURRENT APPLICATION NUMBER: US/09/782,974C
 ; CURRENT FILING DATE: 2002-09-04
 ; PRIOR APPLICATION NUMBER: 60/165,838
 ; PRIOR FILING DATE: 1999-11-16
 ; PRIOR APPLICATION NUMBER: 09/714,449
 ; PRIOR FILING DATE: 2000-11-16
 ; PRIOR APPLICATION NUMBER: 60/198,568
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: 60/166,071
 ; PRIOR FILING DATE: 1999-11-17

Query 61 DFLMICLPCFRTDYLLRRHAWFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 Db 61 DFLMICLPCFRTDYLLRRHAWFGDIPCRVGLFTLAMNRAGSIVFLTVAAADRYFKVHP 120
 Qy 121 HHAVENTISTRVAAGIVCTWLAVLIGTYLQENHLICVQETAVSCSFIMESANGWHDIM 180
 Db 121 HHAVENTISTRVAAGIVCTWLAVLIGTYLQENHLICVQETAVSCSFIMESANGWHDIM 180
 Qy 181 FOLEFFMGLILFCSPKIVWSLRRQOLQARMKTRFIMVAIVFTICLPSVAR 240
 Db 181 FOLEFFMGLILFCSPKIVWSLRRQOLQARMKTRFIMVAIVFTICLPSVAR 240
 Qy 241 LYFLWTVSSACDPSVGAHLITSLFVYFSSPSPKFYNLKICSLKPK 300
 Db 241 LYFLWTVSSACDPSVGAHLITSLFVYFSSPSPKFYNLKICSLKPK 300
 Qy 301 QPGHSKTRQRPEEMPSNIGRRCISVANSFQSOSQGDGWDPHIVEMH 346
 Db 301 QPGHSKTRQRPEEMPSNIGRRCISVANSFQSOSQGDGWDPHIVEMH 346

PRIOR APPLICATION NUMBER: 60/166,678
 PRIOR FILING DATE: 1999-11-19
 PRIOR APPLICATION NUMBER: 60/173,396
 PRIOR FILING DATE: 1999-12-28
 PRIOR APPLICATION NUMBER: 60/184,129
 PRIOR FILING DATE: 2000-02-22
 PRIOR APPLICATION NUMBER: 60/185,421
 PRIOR FILING DATE: 2000-02-28
 PRIOR APPLICATION NUMBER: 60/185,554
 PRIOR FILING DATE: 2000-02-28
 PRIOR APPLICATION NUMBER: 60/186,530
 PRIOR FILING DATE: 2000-03-02
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 192
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 80
 LENGTH: 346
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-282-974C-80

Query Match 100.0%; Score 1853; DB 14; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.6e-163;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCRIEGDTISQMPLLIVAVFVAGNGVALGNGKTRFWKPKSTVYLFNLAVA 60
 Db 1 MYNGSCRIEGDTISQMPLLIVAVFVAGNGVALGNGKTRFWKPKSTVYLFNLAVA 60
 Qy 61 DFLMICLCPFRTDYLRRAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
 Db 61 DFLMICLCPFRTDYLRRAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
 Qy 121 HHAVENTISTRVAGIVCTWLWVILGTYYLLENHLCQETAVSCSFIMESANGHDIM 180
 Db 121 HHAVENTISTRVAGIVCTWLWVILGTYYLLENHLCQETAVSCSFIMESANGHDIM 180
 Qy 181 FOLEFFNPLGILFCSPKIVWSLRRRQLARQARMKATRFIMVAVFPCYLPSYSAR 240
 Db 181 FOLEFFNPLGILFCSPKIVWSLRRRQLARQARMKATRFIMVAVFPCYLPSYSAR 240
 Qy 241 LYFLWTVPSSACDPSVHSGALHTLSFTYMSMLDPLVYFSSPSPKPFYKNUKICSLKPK 300
 Db 241 LYFLWTVPSSACDPSVHSGALHTLSFTYMSMLDPLVYFSSPSPKPFYKNUKICSLKPK 300

RESULT 6
 US-10-079-384-18
 Sequence 18, Application US/10079384
 Publication No. US20030108986A1
 GENERAL INFORMATION:
 APPLICANT: Communi, Didier
 TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
 FILE REFERENCE: 9409/2132
 CURRENT APPLICATION NUMBER: US/10/079,384
 CURRENT FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: US 09/885,453
 PRIOR FILING DATE: 2001-06-20
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 18
 LENGTH: 346
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-079-384-18

Query Match 100.0%; Score 1853; DB 14; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.6e-163;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCRIEGDTISQMPLLIVAVFVAGNGVALGNGKTRFWKPKSTVYLFNLAVA 60
 Db 1 MYNGSCRIEGDTISQMPLLIVAVFVAGNGVALGNGKTRFWKPKSTVYLFNLAVA 60
 Qy 61 DFLMICLCPFRTDYLRRAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
 Db 61 DFLMICLCPFRTDYLRRAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
 Qy 121 HHAVENTISTRVAGIVCTWLWVILGTYYLLENHLCQETAVSCSFIMESANGHDIM 180
 Db 121 HHAVENTISTRVAGIVCTWLWVILGTYYLLENHLCQETAVSCSFIMESANGHDIM 180
 Qy 181 FOLEFFNPLGILFCSPKIVWSLRRRQLARQARMKATRFIMVAVFPCYLPSYSAR 240
 Db 181 FOLEFFNPLGILFCSPKIVWSLRRRQLARQARMKATRFIMVAVFPCYLPSYSAR 240
 Qy 241 OPGHSKTRQRPPEMPISNLGRRCISVANSFOSQSDGWDPHIVEMH 346
 Db 241 OPGHSKTRQRPPEMPISNLGRRCISVANSFOSQSDGWDPHIVEMH 346

RESULT 5
 US-10-188-149A-2
 Sequence 2, Application US/10188149A
 Publication No. US2003007734A1
 GENERAL INFORMATION:
 APPLICANT: YE, Jane et al.
 TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
 TITLE OF INVENTION: RECEPTORS, NUCLEAR ACID MOLECULES ENCODING HUMAN GPCR
 FILE REFERENCE: CLO00782-CON
 CURRENT APPLICATION NUMBER: US/10/188,149A
 CURRENT FILING DATE: 2002-12-10
 PRIOR APPLICATION NUMBER: US 09/666,535
 PRIOR FILING DATE: 2000-09-20
 PRIOR APPLICATION NUMBER: US 60/230,459
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: US 60/192,419
 PRIOR FILING DATE: 2000-03-27
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 346
 TYPE: PRT

; ORGANISM: Homo sapiens
 ; US-10-188-149A-2

Query Match 100.0%; Score 1853; DB 14; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.6e-163;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCRIEGDTISQMPLLIVAVFVAGNGVALGNGKTRFWKPKSTVYLFNLAVA 60
 Db 1 MYNGSCRIEGDTISQMPLLIVAVFVAGNGVALGNGKTRFWKPKSTVYLFNLAVA 60
 Qy 61 DFLMICLCPFRTDYLRRAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
 Db 61 DFLMICLCPFRTDYLRRAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
 Qy 121 HHAVENTISTRVAGIVCTWLWVILGTYYLLENHLCQETAVSCSFIMESANGHDIM 180
 Db 121 HHAVENTISTRVAGIVCTWLWVILGTYYLLENHLCQETAVSCSFIMESANGHDIM 180
 Qy 181 FOLEFFNPLGILFCSPKIVWSLRRRQLARQARMKATRFIMVAVFPCYLPSYSAR 240
 Db 181 FOLEFFNPLGILFCSPKIVWSLRRRQLARQARMKATRFIMVAVFPCYLPSYSAR 240
 Qy 241 OPGHSKTRQRPPEMPISNLGRRCISVANSFOSQSDGWDPHIVEMH 346
 Db 241 OPGHSKTRQRPPEMPISNLGRRCISVANSFOSQSDGWDPHIVEMH 346

RESULT 6
 US-10-079-384-18
 Sequence 18, Application US/10079384
 Publication No. US20030108986A1
 GENERAL INFORMATION:
 APPLICANT: Communi, Didier
 TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
 FILE REFERENCE: 9409/2132
 CURRENT APPLICATION NUMBER: US/10/079,384
 CURRENT FILING DATE: 2002-02-20
 PRIOR APPLICATION NUMBER: US 09/885,453
 PRIOR FILING DATE: 2001-06-20
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 18
 LENGTH: 346
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-079-384-18

Query Match 100.0%; Score 1853; DB 14; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3.6e-163;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCRIEGDTISQMPLLIVAVFVAGNGVALGNGKTRFWKPKSTVYLFNLAVA 60
 Db 1 MYNGSCRIEGDTISQMPLLIVAVFVAGNGVALGNGKTRFWKPKSTVYLFNLAVA 60
 Qy 61 DFLMICLCPFRTDYLRRAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
 Db 61 DFLMICLCPFRTDYLRRAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVHP 120
 Qy 121 HHAVENTISTRVAGIVCTWLWVILGTYYLLENHLCQETAVSCSFIMESANGHDIM 180
 Db 121 HHAVENTISTRVAGIVCTWLWVILGTYYLLENHLCQETAVSCSFIMESANGHDIM 180
 Qy 181 FOLEFFNPLGILFCSPKIVWSLRRRQLARQARMKATRFIMVAVFPCYLPSYSAR 240
 Db 181 FOLEFFNPLGILFCSPKIVWSLRRRQLARQARMKATRFIMVAVFPCYLPSYSAR 240
 Qy 241 LYFLWTVPSSACDPSVHSGALHTLSFTYMSMLDPLVYFSSPSPKPFYKNUKICSLKPK 300

RESULT 7

Db 241 LYFLWTPSSACDPSTGALHTLSPYTMNSMLDPLVYFSSPSPFKP*TKLKICSLKPK 300 ; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 668
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-225-567A-668

Query Match Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCCRIGEDTISQVMPLLVAVFGLGNGVALCGCFHMFCTWKPSVTLFNLAVA 60
Db 1 MYNGSCCRIGEDTISQVMPLLVAVFGLGNGVALCGCFHMFCTWKPSVTLFNLAVA 60

Qy 61 DFLMCLCPPTDYLRRRWAFGDIPCRVGLFTLMNRAGSIVFELTVVADRYFKVHP 120
Db 61 DFLMCLCPPTDYLRRRWAFGDIPCRVGLFTLMNRAGSIVFELTVVADRYFKVHP 120

Qy 121 HHAVNTISTRVAAGIVCTWLVLGTVLLENLICVQETAVSCSFIMESANGWHDIM 180
Db 121 HHAVNTISTRVAAGIVCTWLVLGTVLLENLICVQETAVSCSFIMESANGWHDIM 180

Qy 181 FQLEFFMPGILFCFSRKIVWSLRRQLARQARNKKATRFIMVVAIFITCYLPVSAR 240
Db 181 FQLEFFMPGILFCFSRKIVWSLRRQLARQARNKKATRFIMVVAIFITCYLPVSAR 240

Qy 241 LYFLWTPSSACDPSPVGHALHTISPTYNSMLDPLVYFSSPSPKPYNKLKICSLKPK 300
Db 241 LYFLWTPSSACDPSPVGHALHTISPTYNSMLDPLVYFSSPSPKPYNKLKICSLKPK 300

Qy 301 QPGHSKTRQRPBEMPSNLGRCSRCSVANSFQSQSDQWDPHIVEWH 346
Db 301 QPGHSKTRQRPBEMPSNLGRCSRCSVANSFQSQSDQWDPHIVEWH 346

RESULT 9

Db 61 DFLMCLCPPTDYLRRRWAFGDIPCRVGLFTLMNRAGSIVFELTVVADRYFKVHP 120 ; Sequence 7, Application US/10201481
; Publication No. US20030119024A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: 60/194,701
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO: 2
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-240-842-2

Query Match Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCCRIEGDTISQVMPLLVAVFGLGNGVALCGCFHMFCTWKPSVTLFNLAVA 60
Db 1 MYNGSCCRIEGDTISQVMPLLVAVFGLGNGVALCGCFHMFCTWKPSVTLFNLAVA 60

Qy 61 DFLMCLCPPTDYLRRRWAFGDIPCRVGLFTLMNRAGSIVFELTVVADRYFKVHP 120
Db 61 DFLMCLCPPTDYLRRRWAFGDIPCRVGLFTLMNRAGSIVFELTVVADRYFKVHP 120

Qy 121 HHAVNTISTRVAAGIVCTWLVLGTVLLENLICVQETAVSCSFIMESANGWHDIM 180
Db 121 HHAVNTISTRVAAGIVCTWLVLGTVLLENLICVQETAVSCSFIMESANGWHDIM 180

Qy 181 FQLEFFMPGILFCFSRKIVWSLRRQLARQARNKKATRFIMVVAIFITCYLPVSAR 240
Db 181 FQLEFFMPGILFCFSRKIVWSLRRQLARQARNKKATRFIMVVAIFITCYLPVSAR 240

Qy 241 LYFLWTPSSACDPSPVGHALHTISPTYNSMLDPLVYFSSPSPKPYNKLKICSLKPK 300
Db 241 LYFLWTPSSACDPSPVGHALHTISPTYNSMLDPLVYFSSPSPKPYNKLKICSLKPK 300

Qy 301 QPGHSKTRQRPBEMPSNLGRCSRCSVANSFQSQSDQWDPHIVEWH 346
Db 301 QPGHSKTRQRPBEMPSNLGRCSRCSVANSFQSQSDQWDPHIVEWH 346

RESULT 10

Db 1 MYNGSCCRIGEDTISQVMPLLVAVFGLGNGVALCGCFHMFCTWKPSVTLFNLAVA 60 ; Sequence 7, Application US/10201481
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,968
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO: 7
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-201-481-7

Query Match Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCCRIGEDTISQVMPLLVAVFGLGNGVALCGCFHMFCTWKPSVTLFNLAVA 60
Db 1 MYNGSCCRIGEDTISQVMPLLVAVFGLGNGVALCGCFHMFCTWKPSVTLFNLAVA 60

Qy 61 DFLMCLCPPTDYLRRRWAFGDIPCRVGLFTLMNRAGSIVFELTVVADRYFKVHP 120
Db 61 DFLMCLCPPTDYLRRRWAFGDIPCRVGLFTLMNRAGSIVFELTVVADRYFKVHP 120

Qy 121 HHAVNTISTRVAAGIVCTWLVLGTVLLENLICVQETAVSCSFIMESANGWHDIM 180
Db 121 HHAVNTISTRVAAGIVCTWLVLGTVLLENLICVQETAVSCSFIMESANGWHDIM 180

Qy 121 HHAVNTISTRVAAGIVCTWLVLGTVLLENLICVQETAVSCSFIMESANGWHDIM 180
Db 121 HHAVNTISTRVAAGIVCTWLVLGTVLLENLICVQETAVSCSFIMESANGWHDIM 180

Qy	181	FOLEFFMPGTTILFCSPKIVWSLRRRQLQAROARMKATRFIMVVAIFITCYLPVSAR	240	Db	61	DFLMICLPPFRDYLLRRRHWAFGDIPCRGLFTLANNRAGSIVFLTLYVAADRYFKVYHP	120
Db	181	FOLEFFMPGTLIPLFCSPKIVWSLRRRQLQAROARMKATRFIMVVAIFITCYLPVSAR	240	Qy	121	HHAVENTISTRVAGAVCTVLWALVLTGTVYLLIENHLCQETAVSCSPIMESANGWDIM	180
Qy	241	LYFLWTPSSACDPSVHGALHTLSETYMNSMIDPVYFESSPSRFKYNKLKICSLKP	300	Db	121	HHAVENTISTRVAGAVCTVLWALVLTGTVYLLIENHLCQETAVSCSPIMESANGWDIM	180
Db	241	LYFLWTPSSACDPSVHGALHTLSETYMNSMIDPVYFESSPSRFKYNKLKICSLKP	300	Qy	181	FOLEFFMPGLIILFCSPKIVWSLRRQOLQAROARMKATRFIMVVAIFITCYLPVSAR	240
Qy	301	QPGHSKTRQRPEMPISNLGRSCISVANSFQSQGDGWDPHIVEMH	346	Db	181	FOLEFFMPGLIILFCSPKIVWSLRRQOLQAROARMKATRFIMVVAIFITCYLPVSAR	240
Db	301	QPGHSKTRQRPEMPISNLGRSCISVANSFQSQSDGWDPHIVEMH	346	Qy	241	LYFLWTYPSSACDPSVHGALHTLSETYMNSMIDPVYFESSPSRFKYNKLKICSLKP	300
Db	301	QPGHSKTRQRPEMPISNLGRSCISVANSFQSQSDGWDPHIVEMH	346	Db	241	LYFLWTYPSSACDPSVHGALHTLSETYMNSMIDPVYFESSPSRFKYNKLKICSLKP	300
RESULT 10-278-141-3							
i	Sequence 3,	Application US/10278141			RESULT 11	US-10-321-807-24	
i	Publication No.	US20030138818A1			; Sequence 24, Application US/10321807		
i	GENERAL INFORMATION:				; Publication No. US20030166148A1		
i	APPLICANT: PATTERSON, Chandra				; GENERAL INFORMATION:		
i	APPLICANT: THORNTON, Michael				; APPLICANT: Chen, Rupong		
i	APPLICANT: LU, Yan				; APPLICANT: Dang, Huong T.		
i	APPLICANT: GRAUL, Richard				; APPLICANT: Lowitz, Kevin P.		
i	APPLICANT: KHAN, Farrah A.				; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activate		
i	APPLICANT: GANDHI, Anjeena R.				; TITLE OF INVENTION: Receptors		
i	APPLICANT: WALIA, Narinder K.				; FILE REFERENCE: AREN0086		
i	APPLICANT: NGUYEN, Dannie B.				; CURRENT APPLICATION NUMBER: US/10/321,807		
i	APPLICANT: YUE, Henry				; CURRENT FILING DATE: 2002-12-16		
i	APPLICANT: HAFALIA, April				; PRIOR APPLICATION NUMBER: US/09/714,008		
i	APPLICANT: ELLIOTT, Vicki S.				; PRIOR FILING DATE: 2000-11-16		
i	APPLICANT: LAL, Preeti				; PRIOR APPLICATION NUMBER: 60/1170,496		
i	APPLICANT: REDDY, Roopa				; PRIOR FILING DATE: 1999-11-17		
i	APPLICANT: KALLICK, Deborah A.				; PRIOR APPLICATION NUMBER: 60/1170,496		
i	APPLICANT: TANG, Y. Tom				; PRIOR FILING DATE: 1999-11-17		
i	APPLICANT: AU-YOUNG, Janice				; PRIOR APPLICATION NUMBER: 60/1166,099		
i	TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS				; PRIOR FILING DATE: 1999-11-17		
i	FILE REFERENCE: PI-0096 USA				; PRIOR APPLICATION NUMBER: 60/1166,369		
i	CURRENT APPLICATION NUMBER: US/10/278,141				; PRIOR FILING DATE: 1999-11-17		
i	CURRENT FILING DATE: 2002-10-21				; PRIOR APPLICATION NUMBER: 60/1171,902		
i	PRIOR APPLICATION NUMBER: 60/208,834				; PRIOR FILING DATE: 1999-12-23		
i	PRIOR FILING DATE: 2000-06-02				; PRIOR APPLICATION NUMBER: 60/171,901		
i	PRIOR APPLICATION NUMBER: 60/207,566				; PRIOR FILING DATE: 1999-12-23		
i	PRIOR FILING DATE: 2000-05-25				; PRIOR APPLICATION NUMBER: 60/171,900		
i	PRIOR APPLICATION NUMBER: US01/16285				; PRIOR FILING DATE: 1999-12-23		
i	PRIOR FILING DATE: 2001-05-17				; PRIOR FILING DATE: 2000-02-11		
i	PRIOR APPLICATION NUMBER: 60/205,628				; Remaining Prior Application data removed - See File Wrapper or PALM.		
i	PRIOR FILING DATE: 2000-05-18				NUMBER OF SEQ ID NOS: 133		
i	PRIOR APPLICATION NUMBER: 60/208,861				NUMBER OF SEQ ID NOS: 133		
i	PRIOR FILING DATE: 2000-06-02				SOFTWARE: Perl Program		
i	PRIOR APPLICATION NUMBER: 60/206,222				SEQ ID NO: 24		
i	PRIOR FILING DATE: 2000-05-22				LENGTH: 346		
i	NUMBER OF SEQ ID NOS: 16				TYPE: PRT		
i	SOFTWARE: Perl Program				ORGANISM: Homo sapiens		
i	SEQ ID NO: 3				US-10-321-807-24		
i	LENGTH: 346				FEATURE: misc_feature		
i	TYPE: PRT				NAME/KEY: misc_feature		
i	ORGANISM: Homo sapiens				OTHER INFORMATION: Incyte ID No. US20030138818A1 7474846CD1		
i	FEATURE Match 100.0%	Score 1853; DB 14; Length 346;			US-10-278-141-3		
i	Best Local Similarity 100.0%	Pred. No. 3.6e-163;			Query Match 100.0%; Score 1853; DB 14; Length 346;		
i	Matches 346; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;			Best Local Similarity 100.0%; Pred. No. 3.6e-163;		
i	NAME/KEY: misc_feature	Other INFORMATION: Incyte ID No. US20030138818A1 7474846CD1			Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MYNGSCCRIEGDTISQMPPLLVAVFLGALONGVALGFCFHMTKWPSTYLFNLAVA	60	Qy	1	MYNGSCCRIEGDTISQMPPLLVAVFLGALONGVALGFCFHMTKWPSTYLFNLAVA	60
Db	1	MYNGSCCRIEGDTISQMPPLLVAVFLGALONGVALGFCFHMTKWPSTYLFNLAVA	60	Qy	1	MYNGSCCRIEGDTISQMPPLLVAVFLGALONGVALGFCFHMTKWPSTYLFNLAVA	60
Qy	61	DELMICLPPFRDYLLRRRHWAFGDIPCRGLFTLANNRAGSIVFLTLYVAADRYFKVYHP	120	Db	61	DELMICLPPFRDYLLRRRHWAFGDIPCRGLFTLANNRAGSIVFLTLYVAADRYFKVYHP	120
Db	61	DELMICLPPFRDYLLRRRHWAFGDIPCRGLFTLANNRAGSIVFLTLYVAADRYFKVYHP	120	Qy	61	DELMICLPPFRDYLLRRRHWAFGDIPCRGLFTLANNRAGSIVFLTLYVAADRYFKVYHP	120

Qy 121 HHAVENTISTRVAAGIVCTWLAVLGLTVYLLENHICVQETAVSCSFIMESANGHIDM 180
Db 121 HHAVENTISTRVAAGIVCTWLAVLGLTVYLLENHICVQETAVSCSFIMESANGHIDM 180

Qy 181 FOLEFFMPGILIFCSPKIVWSLRROQLARQARMKKATRFIMMVAVFPTCYLPVSAR 240
Db 181 FOLEFFMPGILIFCSPKIVWSLRROQLARQARMKKATRFIMMVAVFPTCYLPVSAR 240

Qy 241 LYFLWTVPSACDPSVGAHLHTLSFTYFNSMMLDPLYYFSSPSPKPKYNKLKICSLKPK 300
Db 241 LYFLWTVPSACDPSVGAHLHTLSFTYFNSMMLDPLYYFSSPSPKPKYNKLKICSLKPK 300

Qy 301 QPGHSKTRQRPEEMPISNIGRCSRISVANSFSQSOGDGMWPHIVEH 346
Db 301 QPGHSKTRQRPEEMPISNIGRCSRISVANSFSQSOGDGMWPHIVEH 346

RESULT 12

Sequence 2, Application US/10076260
Publication No. US20030171541A1

GENERAL INFORMATION:

APPLICANT: Elliott, Steven G.
APPLICANT: Rogers, No. US20030171541A1
APPLICANT: Busse, Leigh Anne

TITLE OF INVENTION: G-Protein Coupled Receptor Molecules and Uses Thereof

FILE REFERENCE: 02-076

CURRENT APPLICATION NUMBER: US/10/076,260

PRIOR APPLICATION NUMBER: 2002-02-14

PRIOR FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 22

SEQ ID NO 2

SOFTWARE: Patentin Ver. 2.0

LENGTH: 346

TYPE: PRT

ORGANISM: Homo sapiens

us-10-076-260-2

Query Match Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCCPIEGGTISQVMPPLLIIVAFULGALGNQVALCFCEHMCKTKPSTVYLFNLAVA 60
Db 1 MYNGSCCPIEGGTISQVMPPLLIIVAFULGALGNQVALCFCEHMCKTKPSTVYLFNLAVA 60

Qy 61 DFLMICPFRDYIYLRRHWAFGDIPIORVGLFTLAMNRASSIVELTVADRYFKVHP 120
Db 61 DFLMICPFRDYIYLRRHWAFGDIPIORVGLFTLAMNRASSIVELTVADRYFKVHP 120

Qy 121 HHAVENTISTRVAAGIVCTWLAVLGLTVYLLENHICVQETAVSCSFIMESANGHIDM 180
Db 121 HHAVENTISTRVAAGIVCTWLAVLGLTVYLLENHICVQETAVSCSFIMESANGHIDM 180

Qy 181 FOLEFFMPGILIFCSPKIVWSLRROQLARQARMKKATRFIMMVAVFPTCYLPVSAR 240
Db 181 FOLEFFMPGILIFCSPKIVWSLRROQLARQARMKKATRFIMMVAVFPTCYLPVSAR 240

Qy 241 LYFLWTVPSACDPSVGAHLHTLSFTYFNSMMLDPLYYFSSPSPKPKYNKLKICSLKPK 300
Db 241 LYFLWTVPSACDPSVGAHLHTLSFTYFNSMMLDPLYYFSSPSPKPKYNKLKICSLKPK 300

Qy 301 QPGHSKTRQRPEEMPISNIGRCSRISVANSFSQSOGDGMWPHIVEH 346
Db 301 QPGHSKTRQRPEEMPISNIGRCSRISVANSFSQSOGDGMWPHIVEH 346

RESULT 13

Sequence 2, Application US/10044643
Publication No. US20030195335A1

GENERAL INFORMATION:

APPLICANT: Kumud
APPLICANT: Verne, Corine
APPLICANT: Casman, Stacie J
APPLICANT: Wolenc, Adam R
APPLICANT: Spaderna, Steven K
APPLICANT: Padigaru, Muradihara
APPLICANT: Misrau, Vishnu S
APPLICANT: Tchernov, Velizar T
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Baumgartner, Jason C
APPLICANT: Gushev, Vladimir
TITLE OF INVENTION: No. US20030195335A1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-749
CURRENT APPLICATION NUMBER: US/10/044,643
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 60/193,664
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 60/194,614
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,063
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,066
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,067
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,068
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,069
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,070
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,071
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,072
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/219,855
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/221,284
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/221,325
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/224,588
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/239,613
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 60/262,508
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/263,604
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,433
PRIOR FILING DATE: 2001-01-23
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens

US-10-044-643-2

Query Match Score 1853; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCCPIEGGTISQVMPPLLIIVAFULGALGNQVALCFCEHMCKTKPSTVYLFNLAVA 60
Db 1 MYNGSCCPIEGGTISQVMPPLLIIVAFULGALGNQVALCFCEHMCKTKPSTVYLFNLAVA 60

Qy 61 DFLMICPFRDYIYLRRHWAFGDIPIORVGLFTLAMNRASSIVELTVADRYFKVHP 120
Db 61 DFLMICPFRDYIYLRRHWAFGDIPIORVGLFTLAMNRASSIVELTVADRYFKVHP 120

Qy 121 HHAVENTISTRVAAGIVCTWLAVLGLTVYLLENHICVQETAVSCSFIMESANGHIDM 180
Db 121 HHAVENTISTRVAAGIVCTWLAVLGLTVYLLENHICVQETAVSCSFIMESANGHIDM 180

Qy 181 FOLEFFMPGILIFCSPKIVWSLRROQLARQARMKKATRFIMMVAVFPTCYLPVSAR 240
Db 181 FOLEFFMPGILIFCSPKIVWSLRROQLARQARMKKATRFIMMVAVFPTCYLPVSAR 240

Qy 241 LYFLWTVPSACDPSVGAHLHTLSFTYFNSMMLDPLYYFSSPSPKPKYNKLKICSLKPK 300
Db 241 LYFLWTVPSACDPSVGAHLHTLSFTYFNSMMLDPLYYFSSPSPKPKYNKLKICSLKPK 300

Qy 301 QPGHSKTRQRPEEMPISNIGRCSRISVANSFSQSOGDGMWPHIVEH 346
Db 301 QPGHSKTRQRPEEMPISNIGRCSRISVANSFSQSOGDGMWPHIVEH 346

RES

Qy 121 HHAVENTISTRAAVICVCTLWALVILGTYYLLENHLCVQETAVSCSSEFIMSSANGWHIDM 180
 Db 121 HHAVENTISTRAAVICVCTLWALVILGTYYLLENHLCVQETAVSCSSEFIMSSANGWHIDM 180

Qy 181 FOLEFFMPLGILIFCSPKIVWSLRQQLARQARMKKATRFIMVVAIFITCYLPVSAR 240
 Db 181 FOLEFFMPLGILIFCSPKIVWSLRQQLARQARMKKATRFIMVVAIFITCYLPVSAR 240

Qy 241 LYFLWTVPSACDPSVHGALHITSLPTYMSMLDPVLYFESSPSPPKFYNLKICSLKPK 300
 Db 241 LYFLWTVPSACDPSVHGALHITSLPTYMSMLDPVLYFESSPSPPKFYNLKICSLKPK 300

Qy 301 QPGHSKTRQRPEEMPISNLGRSCISVANSFOSQSDGQWDPHIVEWH 346
 Db 301 QPGHSKTRQRPEEMPISNLGRSCISVANSFOSQSDGQWDPHIVEWH 346

Db 301 QPGHSKTRQRPEEMPISNLGRSCISVANSFOSQSDGQWDPHIVEWH 346

RESULT 15
 US-10-210-172-178
 ; Sequence 178, Application US/10210172
 ; Publication No. US2004043928A1

; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: PATTERSON, Chandra
 ; APPLICANT: LU, Dvyng Aina M.
 ; APPLICANT: THORNTON, Michael
 ; APPLICANT: LU, Yan
 ; APPLICANT: TRIBOUTEY, Catherine M.
 ; APPLICANT: GRAUL, Richard
 ; APPLICANT: KHAN, Farrah A.
 ; APPLICANT: GANDHI, Ameena R.
 ; APPLICANT: WALIA, Narinder K.
 ; APPLICANT: NGUYEN, Darniel B.
 ; APPLICANT: YUB, Henry
 ; APPLICANT: HAFALIA, April
 ; APPLICANT: ELLIOTT, Vicki S.
 ; APPLICANT: LAL, Preeti
 ; APPLICANT: REDDY, Roopa
 ; APPLICANT: KALLICK, Deborah A.
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: AU-YOUNG, Janice
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: PI-0096 PCT
 ; CURRENT APPLICATION NUMBER: US/10/296, 081
 ; PRIORITY APPLICATION NUMBER: 60/205,628; 60/206,222; 60/207,566; 60/208,834; 60/208, 861
 ; PRIORITY FILING DATE: 2000-05-18; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 3
 ; LENGTH: 346
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030220477A1 7474846CD1
 US-10-296-081-3

Query Match 100.0%; Score 1853; DB 15; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3..6e-13;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCCRIEGDTISQVNMPPLLIVAFVLGALGNGVVALCGFCFHMKTKWPSTYLFNIAVA 60
 Db 1 MYNGSCCRIEGDTISQVNMPPLLIVAFVLGALGNGVVALCGFCFHMKTKWPSTYLFNIAVA 60

Qy 61 DFLIMICLPRTDYLLRRHWAEGDIPCRVGLFTLAMNRAGSTIVELTVTAADRYFKVWHP 120
 Db 61 DFLIMICLPRTDYLLRRHWAEGDIPCRVGLFTLAMNRAGSTIVELTVTAADRYFKVWHP 120

Qy 121 HHAVENTISTRAAVICVCTLWALVILGTYYLLENHLCVQETAVSCSSEFIMSSANGWHIDM 180
 Db 121 HHAVENTISTRAAVICVCTLWALVILGTYYLLENHLCVQETAVSCSSEFIMSSANGWHIDM 180

```

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 327
; SOFTWARE: CuraSeclist version 0.1
; SEQ ID NO: 178
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-210-172-178

Query Match 100.0%; Score 1853; DB 15; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.6e-163; Mismatches 0; Indels 0; Gaps 0;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYNGSCCRIEGDTISQWPPLIVAFVGLNGVALGFCFHMKTWKPSTVLFNLA 60
Db 1 MYNGSCCRIEGDTISQWPPLIVAFVGLNGVALGFCFHMKTWKPSTVLFNLA 60
Qy 61 DFLIMICLPIERTDYLLRHWAFGDIPIRGVLFTLAMNRAGSIVELTVAA 120
Db 61 DFLIMICLPIERTDYLLRHWAFGDIPIRGVLFTLAMNRAGSIVELTVAA 120
Qy 121 HRAVNTISTRVAAGIVCTWLAVLVLGTWYLLLENHLCVQETAVSCSFIMESANGHDIM 180
Db 121 HRAVNTISTRVAAGIVCTWLAVLVLGTWYLLLENHLCVQETAVSCSFIMESANGHDIM 180
Qy 181 FQLEFFMPMLGLIILFCSFKIVWSLRROQLARQARMKATRFIMVAVFITYCLPSVSR 240
Db 181 FQLEFFMPMLGIILFCSFKIVWSLRROQLARQARMKATRFIMVAVFITYCLPSVSR 240
Qy 241 LYFLWTVPSACDPSVHGRGALHTLSFTYTMNSMLDPLVYYFSSSPSPKFKYNKLKICSLKPK 300
Db 241 LYFLWTVPSACDPSVHGRGALHTLSFTYTMNSMLDPLVYYFSSSPSPKFKYNKLKICSLKPK 300
Qy 301 QPHSKTKTORPEEMPISNIGRRSCTSVANSFOQSODGMDPHIVEWH 346
Db 301 QPHSKTKTORPEEMPISNIGRRSCTSVANSFOQSODGMDPHIVEWH 346

```

Search completed: August 30, 2005, 18:38:12
 Job time : 164 secs

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:
1: uniprot_sprot:
2: uniprot_trembl:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1833	100.0	346	1	GPR81_HUMAN	Q9bxco homo sapien
2	1841	99.4	346	2	Q6NAT5	Q9bxco homo sapien
3	1483	80.0	343	1	GP81_MOUSE	Q9bxco homo sapien
4	883.5	47.7	363	2	Q8TD54	Q9bxco homo sapien
5	881.5	47.6	387	1	Q8NGE4	Q9bxco homo sapien
6	880.5	47.5	387	1	G09B_HUMAN	Q9bxco homo sapien
7	868.5	46.9	360	2	Q9EPF6	Q9bxco homo sapien
8	862.5	46.5	360	2	Q80239	Q9bxco rattus norvegicus
9	996	32.2	263	2	Q8NGV8	Q9bxco homo sapien
10	529	28.5	384	2	Q8NGW4	Q9bxco homo sapien
11	529	28.5	384	2	Q8WP7	Q9bxco homo sapien
12	529	28.5	423	2	Q8TD55	Q9bxco homo sapien
13	450.5	24.3	319	2	Q9NQ20	Q9bxco homo sapien
14	446.5	24.1	319	1	GP31_HUMAN	Q9bxco homo sapien
15	446.5	24.1	319	1	Q9JUS1	Q9bxco homo sapien
16	375.5	20.3	309	2	Q8R328	Q9bxco mus musculus
17	371.5	20.0	309	1	CLT2_MOUSE	Q9bxco mus musculus
18	366.5	19.8	346	1	CLT2_HUMAN	Q9bxco homo sapien
19	364	19.6	362	1	P2YR_CHICK	P34996 Gallus gallus
20	364	19.6	373	1	P2YR_MELGSA	P49652 meleagris gallopavo
21	362.5	19.6	373	1	P2YR_BOVIN	P48042 bos taurus
22	352	19.5	345	1	CLT2_PIG	Q9503 sus scrofa
23	352	19.3	373	1	P2YR_RAT	P49651 rattus norvegicus
24	356.5	19.2	373	1	P2YR_CAVPO	P52902 cavia porcellus
25	355.5	19.2	309	1	CLT2 RAT	Q92459 rattus norvegicus
26	354	19.1	373	1	P2YR_HUMAN	P47900 homo sapiens
27	351.5	19.0	373	1	P2YR_MOUSE	P49650 mus musculus
28	351.5	19.0	390	2	Q8QQ4	Q869q4 carassius auratus
29	348.5	18.9	373	2	Q6NSP5	Q6nsps5 homo sapiens
30	348.5	18.8	373	2	Q8BNJ5	Q8bnj5 mus musculus
31	346.5	18.7	370	1	P2Y9_HUMAN	Q93677 homo sapiens

Nice hit
RESULT 1 KIRICHI \sim B3

RESULT 1 KIRICHI \sim B3
GP81_HUMAN STANDARD; PRT: 346 AA.

ID: GP81_HUMAN
ID: Q9BXCO;
AC: 09BXCO;
DT: 10-OCT-2003 (Rel. 42, Created)
DT: 10-OCT-2003 (Rel. 42, Last sequence update)
DT: 25-OCT-2004 (Rel. 45, Last annotation update)
DB: Probable G protein-coupled receptor (GPR81) (FKSG80 protein)

GN: Name=GPR81; Synonyms=FKSG80;
Homo sapiens (Human);
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC: NCBI_TaxID=9606;
OX: NCBI_TaxID=9606;

RN: RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;
RA: Lee D.K., Nguyen T., Lynch K.R., Chang R., Vanti W.B., Arkhitko O.,
RA: Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT: "Discovery and mapping of ten novel G protein-coupled receptor genes.",
RN: Gene 275:83-91(2001).
RL: [2]
RN: SEQUENCE FROM N.A.
RX: MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;
RA: Takeda S., Kadovari S., Haga T., Takaesu H., Mitaku S.;
RT: "Identification of G protein-coupled receptor genes from the human genome sequence";
RL: FEBS Lett. 520:97-101 (2002).
RN: [3]
RN: SEQUENCE FROM N.A.
RA: Wang Y.-G., Gong L.;
RT: "Molecular cloning of FKSG80, a novel gene encoding a putative chemokine receptor";
RN: Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL: [4]
RN: SEQUENCE FROM N.A.
RA: Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT: "Genome-wide discovery and analysis of human seven transmembrane helix receptor genes";
RL: Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC: -1- FUNCTION: Orphan receptor.
CC: -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC: -1- TISSUE SPECIFICITY: Expressed in pituitary tissue. Not detected in frontal, temporal and occipital lobes of the cortex, basal forebrain, caudate nucleus, nucleus accumbens, and hippocampus.
CC: -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC: This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/

RN	[4] SEQUENCE FROM N.A.	DR EMBL; AB065865; BAC0608.1; -.
RP	Sato T., Okouchi I., Arita M., Futami K., Matsumoto S., Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S., Tsutsumi S., Aburatani H., Asai K., Akiyama Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.	DR GO; 0016021; C:integral to membrane; IEA.
RA	-I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).	DR GO; 0045028; P:purinergic nucleotide receptor activity; IEA.
RL	-I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	DR GO; 0001584; P:rhodopsin-like receptor activity; IEA.
CC	DR InterPro; IPR002286; P:G-protein coupled receptor protein signalin.	DR GO; 0007186; P:G-protein coupled receptor protein signalin.
CC	DR InterPro; IPR002286; P2_purnocptor.	DR InterPro; IPR002286; P2_purnocptor.
EMBL	EMBL; AB149894; BAC061621; -.	DR PF00001; 7tm1; 1.
EMBL	EMBL; AB065876; BAC06094.1; -.	DR PRINTS; PR00237; GPCCRHDOPSN.
GO	GO; 0016021; C:integral to membrane; IEA.	DR PRINTS; PR01157; PYPPURNCPTR.
DR	DR PROSITE; PS00237; G:PROTEIN_RECV_P1_1; 1.	DR PROSITE; PS00237; G:PROTEIN_RECV_P1_2; 1.
GO	GO; 0045028; P:purinergic nucleotide receptor activity; IEA.	DR PROSITE; PS50262; G:PROTEIN_RECV_P1_2; 1.
GO	GO; 0004872; P:receptor activity; IEA.	DR G-protein coupled receptor; Receptor: Transmembrane.
DR	DR GO; 0001584; P:rhodopsin-like receptor activity; IEA.	KW SQ SEQUENCE 387 AA; 44495 MW; 26433C835E85EC81 CRC64;
DR	DR GO; 0002186; P:G-protein coupled receptor protein signalin.	Query Match 47.6%; Score 881.5; DB 2; Length 387;
InterPro	IPR000276; GPCR_Rhodpsn.	Best Local Similarity 52.2%; Pred. No. 3.6e-54;
InterPro	IPR002286; P2_purnocptor.	Mismatches 107; Indels 7; Gaps 4;
pfam	PF00001; 7tm1; 1.	Matches 178; Conservative 49; Mismatches 107; Indels 7; Gaps 4;
DR	DR PRINTS; PR00237; GPCCRHDOPSN.	Qy 5 SCCRIEGDTISQMPPLILIVAFVLAIGNGVAGLCFCPEKIMKTKRSTVYLFNLAYADELL 64
DR	DR PROSITE; PS00237; G:PROTEIN_RECV_P1_1; 1.	Db 17 NCCVFRDDEFAKVLPEVGLFEGFLNLGNGLALNFCFLKWSRSRIFLNLADEFLL 76
KW	G-protein coupled receptor; Receptor: Transmembrane.	Qy 65 MICLPPRTDYLLRRHAWFGDIPCRVGLFLAMNAGASIVFLTVAADRVFKVDPVPHAV 124
SQ	SQ SEQUENCE 363 AA; 41849 MW; C4B0BEC9CCB81D56 CRC64;	Db 77 FICLPTMMDYYVRSDWKEFDPICPVLFLAMNAGASIVFLTVAADRVFKVDPVPHAV 136
Query Match 47.7%; Score 883.5; DB 2; Length 363;	Qy 125 NTISTRVAAGIVCTLVLLWLTGTVLLNLCVQETAVSCESFIMESANGWHDIMFOLE 125	
Best Local Similarity 52.8%; Pred. No. 2.5e-54;	Db 137 NKISWNTAAISCLLWLTGTVLLKLKULLQINGPANCISFSICHTPFWHEAMFLLE 196	
Matches 180; Conservative 47; Mismatches 107; Indels 7; Gaps 4;	Qy 185 FMPMLGLILEFCSEKTVWSLRQRQLARQAMKKATPRIMVVAIFITCYLPSVSPARLYFL 244	
Qy	Qy 17 NCCVFRDDEFAKVLPEVGLFEGFLNLGNGLALNFCFLKWSRSRIFLNLADEFLL 76	Db 197 FLLPLGTLFPLCSARLWLSURQR-QMDRHAKIKRATIFIMVVAIVFVCFPSVVVRIRIF 255
Db	Db 65 MICLPPRTDYLLRRHAWFGDIPCRVGLFLAMNAGASIVFLTVAADRVFKVDPVPHAV 124	Qy 245 WTPVSSA---CD--PVGVRGHITISFTYNSMLDPLVYVFSSPSPKPVNKLKICSLKP 299
Qy	Db 77 IICLPLFLMDNYTTRWDWFGDIPCRMLMFLAMNRQSSIIIFTWAVDRYPRVPHHAL 136	Db 256 WILHTSGTQNCEVYVSVDAFFPITTSFTYNSMLPVVYFFFSPPNFSTLINRCQLR 315
Db	Qy 125 NTISTRVAAGIVCTLVLLWLTGTVLLNLCVQETAVSCESFIMESANGWHDIMFOLE 184	Qy 300 KQPGHSKSTORPEEMPTSNLGRRSCTISVANSFQSODGQWDP 340
Db	Db 137 NKISWNTAAISCLLWLTGTVLLKLKULLQINGPANCISFSICHTPFWHEAMFLLE 196	Db 316 KMTGEPDNNRSTSVELGDPNKT-RGAPEALMANSGEWPWSP 355
Qy	Qy 185 FMPMLGLILEFCSEKTVWSLRQRQLARQAMKKATPRIMVVAIFITCYLPSVSPARLYFL 244	RESULT 6
hb	hb 197 FFLPLGTLFPLCSARLWLSURQR-QMDRHAKIKRATIFIMVVAIVFVCFPSVVVRIRIF 255	GN Homo_sapiens (Human); Synonyms=HM74;
Qy	Qy 245 WTPVSSA---CD--PVGVRGHITISFTYNSMLDPLVYVFSSPSPKPVNKLKICSLKP 299	OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; OC Eukaryota; Metazoa; OC Mammalia; Buteraria; Primates; Hominidae; Homo.
Db	Db 256 WILHTSGTQNCEVYVSVDAFFPITTSFTYNSMLPVVYFFFSPPNFSTLINRCQLR 315	ID G09159; HUMAN ID G09159; HUMAN STANDARD; PRT; 387 AA.
Qy	Qy 300 KQPGHSKSTORPEEMPTSNLGRRSCTISVANSFQSODGQWDP 340	AC P49013; ID G09159; HUMAN
Db	Db 316 KMTGEPDNNRSTSVELGDPNKT-RGAPEALMANSGEWPWSP 355	DT 01-FEB-1996 (Rel. 33, Created)
DE	DE Seven transmembrane helix receptor.	DT 01-FEB-1996 (Rel. 33, Last sequence update)
OS	OS Homo sapiens (Human)	DT 25-OCT-2004 (Rel. 45, Last annotation update)
OC	OC Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.	DB Probable G protein-coupled receptor GPR109B (G protein-coupled receptor HM74).
NCBI	NCBI TaxID=9606;	DE DE receptor HM74).
RN	RN [1]	GN Name=GPR109B; Synonyms=HM74;
RP	RP SEQUENCE FROM N.A.	OS Homo sapiens (Human);
QBNGE4	QBNGE4 PRELIMINARY; PRT; 387 AA.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Buteraria; Primates; Hominidae; Homo.
AC	AC DT 01-OCT-2002 (TREMBLrel. 22, Created)	AC P49013; ID G09159; HUMAN
DT	DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)	DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT	DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE	DE Seven transmembrane helix receptor.	DT 25-OCT-2004 (Rel. 45, Last annotation update)
OS	OS Homo sapiens (Human)	DB Probable G protein-coupled receptor GPR109B (G protein-coupled receptor HM74).
OC	OC Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.	DE DE receptor HM74).
NCBI	NCBI TaxID=9606;	GN Name=GPR109B; Synonyms=HM74;
RN	RN [1]	OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; OC Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
RP	RP SEQUENCE FROM N.A.	AC P49013; ID G09159; HUMAN
RA	RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.	DT 01-FEB-1996 (Rel. 33, Last sequence update)
RL	RL -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).	DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC	CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	DB Probable G protein-coupled receptor GPR109B (G protein-coupled receptor HM74).
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -	DT 01-FEB-1996 (Rel. 33, Last sequence update)

the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
CC	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
CC	Putative seven transmembrane spanning receptor.
CC	Name=spri9b; Synonyms=Puma-g, Pumag;
CC	Mus musculus (Mouse)
CC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC	NCBI_TaxID=10909;
DR	[1]
DR	RN
DR	SEQUENCE FROM N.A.
DR	STRAIN=129/SVJ, and C57BL/6;
DR	RC
DR	Schaub A., Futterer A., Preffer K.;
DR	RA
DR	Submitted (NOV-2000) to the ENB/GenBank/DDJB databases.
DR	RL
DR	-SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR	CC
DR	-SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR	DR
DR	EMBL; AJ300199; CAC17791.1; -.
DR	DR
DR	EMBL; AJ300198; CAC17790.1; -.
DR	DR
DR	MGI; 1933338; Gpr109b.
DR	DR
DR	GO; GO:0016021; C:integral to membrane; IDA.
DR	DR
DR	GO; GO:000525; F:GTP binding; IDA.
DR	DR
DR	GO; GO:001614; F:purinergic nucleotide receptor activity; IDA.
DR	DR
DR	InterPro; IPR000276; GPCR_Rhodopsn.
DR	DR
DR	PFAM; PF00001; 7tm_1; 1.
DR	DR
DR	PRINTS; PRO0237; GPCR_RHODOPSN.
DR	DR
DR	PROSITE; PS00237; G-PROTEIN RECEP_F1_1; 1.
DR	DR
DR	PROSITE; PS00237; G-PROTEIN RECEP_F1_2; 1.
DR	DR
DR	KW
DR	G-protein coupled receptor; Transmembrane.
DR	DR
DR	SEQUENCE 360 AA; CCBS52A247577FC CRC64;
FT	Query Match
FT	Score 46.9%; Score 868.5%; DB 2; Length 360;
FT	Best Local Similarity 55.6%; Pred. No. 2.8e-53;
FT	Matches 178; Conservative 39; Mismatches 96; Indels 7; Gaps 4;
FT	QY
FT	3 NG-SCCRIEGDTISQMPPLIVAFVIGALGNGVALCQFCPHMKTKPSTVYLFLNLAVAD 61
FT	DB
FT	11 NGKNCUCVFRDENIAKVLPPVGLFEPVGLNGLALWIPCHLKSMSKSSRFLNLAVAD 70
FT	FT
FT	62 FLIMICLPLFRTDYYLRRRHWAEGDIPCRVGLFTLAMNRAGSIVFELTVAAADRYFKVYHHP 121
FT	QY
FT	71 FLLMICLPLFRTDYYLRRRHWAEGDIPCRVGLFTLAMNRAGSIVFELTVAAADRYFKVYHHP 130
FT	DB
FT	122 HAVNTIISTRVAGIVCTLWALVLTGTYLLENHLCVQETAVSCSPIMESANGWHDIMF 181
FT	DB
FT	131 HELNKISNRATAISCLFWLGTIGTVLHYTNMNTKONGEAYLCSSESFSICYNERFDAMF 190
FT	FT
FT	182 QLEFFMPGLGILFCFSFXIVWSLRROOLARQARMKATRFIMVAVTFITCYLPVSARL 241
FT	DB
FT	191 LLEBFPLLAIFLFCGRIIWSRQR_QMDRHKAKRINAIFIMVAVTFICLPLSVAVRI 249
FT	FT
FT	242 YPLWTPS--SACD--PSVHGALHTLSFTYMNNSMIDLPLAAYFSSPSFPKEYNLUKICS 296
FT	DB
FT	250 RIFWLLYYKVNTRNCDISSVSDLAFTTLSFTYMNNSMIDLPVYYFSSPSFPNEFTCINRC 309
FT	FT
FT	297 LKPQKPEPSKQTORPENMP 316
FT	DB
FT	310 LKKTGLQEPDNNRSTSYBLT 329
FT	GN
FT	Name=fM74b;
FT	Rattus norvegicus (Rat).
FT	OC
FT	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
FT	[1]
FT	RN
FT	SEQUENCE FROM N.A.
RESULT	8
Q80Z39	PRELIMINARY;
ID	PRT; 360 AA.
Q80Z39	AC
Q80Z39	DT 01-JUN-2003 (TREMBLrel. 24, Created)
Q80Z39	DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
Q80Z39	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Q80Z39	DE Nicotinic acid receptor.
Q80Z39	OS Name=fM74b;
Q80Z39	Rattus norvegicus (Rat).
Q80Z39	OC
Q80Z39	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Q80Z39	[1]
Q80Z39	RN
Q80Z39	SEQUENCE FROM N.A.
Q9BP66	PRELIMINARY;
ID	PRT; 360 AA.
Q9BP66	AC
Q9BP66	DT 01-MAR-2001 (TREMBLrel. 16, Created)
Q9BP66	DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
Q9BP66	DE Nicotinic acid receptor.
Q9BP66	OS Name=fM74b;
Q9BP66	Rattus norvegicus (Rat).
Q9BP66	OC
Q9BP66	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Q9BP66	[1]
Q9BP66	RN
Q9BP66	SEQUENCE FROM N.A.

Query Match 24.2%; Score 4.8.5.; Pred. No. 8.1e-14; Mismatches 121; Indels 11; Gaps 5;

Best Local Similarity 34.0%; Matches 100; Conservative 62; N-Linker 5; Score 4.8.5.; Length 319;

Query 7 CRIEGDTISQVMPLILIVAFVLGALNGVALCGFCFHMKWPKSTVYLFLNLAVALADFLIMI 66

Db 6 CSAPSTVATAVGVLGLBECGIGLGNNAVALWFLFVRWKPAVYLNALADLLAA 65

Query 67 CLPFRTDYLRRRHWAGDIPCRVGLFLAMNRAGSLVFLTVAAODYKTHPHHAVENT 126

Db 66 CLPFLAAFLYSLQAHMIGRVGCAWLRLFDLRSRVGAFLAVAVDRLRVVHPRLKVNLI 125

Query 127 ISTRVAAGIVCTWLVLYTGLTYLLENHLCKVQETAVSCESTIMEANG----WHIDMF 181

Db 128 LSPQAALGSVGLWLLWVWALTCPLLSE--AAQNSTRCHSE--YSRADGFSIIWQEALS 182

Query 182 QLEFFMPGIIIFCSFKIVWSLRRR--QOLARQARMKKATRFIMVVAIVFITYLPSVSAR 240

Db 183 CLQFLVLPGLIVFCNAGIRALQKRUREPEKQPKLQPAQALYTLLVFLCFLPCFLAR 242

Query 241 -LYFLWTVPSACDPSVGHMHTLSFTYMSMLDPVYYFSSPSPKFVNKL 292

Db 243 VLMHIFQNLGSCLACAWAHTSDVTGSLTYLHSVNVNPVYCFSSPFRSSYRRV 296

Search completed: August 30, 2005, 18:33:48
Job time : 175 secs

RESULT 15

Q9JLS1 PRELIMINARY; PRT; 319 AA.

ID Q9JLS1 ID: Q9JLS1 PRELIMINARY; PRT; 319 AA.

AC Q9JLS1 AC: Q9JLS1 PRELIMINARY; PRT; 319 AA.

DT 01-OCT-2000 DT: 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-MAR-2004 DT: 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

.DE G protein coupled receptor.

GN Name=Rp10C; OS Mus musculus (Mouse); OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090 [1]

RN SEQUENCE FROM N A. RQ MEDLINE-99411663; PubMed=10501965;

RA Schimenti J.C.; RT "ORFless, intronless, and mutant transcription units in the mouse t complex respond ('Tcr') locus." RL Mamm. Genome 10:669-676 (1999).

DR EMBL; PAF140708; PAF26668.1; -. DR MGI:98543; Top10C.

DR GO:GO-0016021; C:integral membrane; IEA.

DR GO:GO-0004812; F:receptor activity; IEA.

DR GO:GO-001584; P:rhodopsin-like receptor activity; IEA.

DR GO:GO-000786; B:G-protein coupled receptor protein signalin. . .; IEA.

DR InterPro; IPR000776; GPCR_Rhodopen.

DR Pfam; PF0001; 7cm1; 1.

DR PRINTS; PR00237; GPCR_RHODOPSN.

DR PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1; UNKNOWN_1.

DR PROSITE; PS50262; G PROTEIN_RECEP_F1_2; 1.

KW Receptor.

SEQUENCE 319 AA; 35551 MW; 571F6FB485BD7C4 CRC64;

Query Match 24.1%; Score 4.46.5.; DB 2; Length 319;

Best Local Similarity 32.5%; Matches 104; Conservative 64; N-Linker 6; Score 4.46.5.; Length 319;

Db 6 CSAASTVVAETVMTLITBCVGLMGNAVALWFLFYRKWKPAYVLFNLVYADLLAT 65

Query 7 CRIEGDTISQVMPLILIVAFVLGALNGVALCGFCFHMKWPKSTVYLFLNLAVALADFLIMI 66

THIS PAGE BLANK (USPTO)